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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-030-606-110.res made by tport on Thu 1 May 103 14:49:36-PDT.

Query sequence being compared: US-09-030-606-110 (1-3410)
Number of sequences searched: 410
Number of scores above cutoff: 410

Results of the initial comparison of US-09-030-606-110 (1-3410) with:

- File : 6130043.seq
- File : 6252047.seq
- File : US08806596.seq
- File : US08850713.seq
- File : US08904809.seq
- File : US09020747.seq
- File : US09841894A.seq

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SCORE 0

STDEV

1 2 3 4 5 6 7 8 9

Similarity matrix

Mismatch penalty

Gap penalty

Gap size penalty

Cutoff score

Randomization group

Unitary

K-tuple

Joining penalty

Window size

SEARCH STATISTICS

Mean

Median

Standard Deviation

Scores:

Mean

Median

Standard Deviation

76

41

185.74

2652

2273

1894

1516

1137

758

1379

2730

3031

3410

4

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500

0.33

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Times:

CPU

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189792

410

410

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Length	Score	Init. Opt.	Frame
1. US-09-020-747-11	Sequence 110, Application	3410	3410	3410	17.95 0

The list of other best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Frame
2. US-08-850-713-16	Sequence 16, Application	2154	1735	2130	8.93 0
3. US-09-071-710-16	Sequence 16, Application	2152	1501	2144	7.67 0
4. US-09-525-397-16	Sequence 16, Application	2152	1501	2144	7.67 0
5. US-09-841-894A-1	Sequence 16, Application	2152	1501	2144	7.67 0
6. US-09-071-710-15	Sequence 15, Application	2143	1381	2129	7.03 0
7. US-09-525-397-15	Sequence 15, Application	2143	1381	2129	7.03 0
8. US-09-841-894A-1	Sequence 15, Application	2143	1381	2129	7.03 0
9. US-08-806-596-10	Sequence 10, Application	789	560	720	2.61 0
10. US-08-904-809-10	Sequence 10, Application	789	554	720	2.57 0
11. US-09-020-747-10	Sequence 10, Application	789	554	720	2.57 0
12. US-09-071-710-12	Sequence 12, Application	294	291	291	1.16 0
13. US-09-525-397-12	Sequence 12, Application	294	291	291	1.16 0
14. US-09-841-894A-1	Sequence 12, Application	294	291	291	1.16 0
15. US-09-071-710-10	Sequence 10, Application	288	287	287	1.14 0
16. US-09-525-397-10	Sequence 10, Application	288	287	287	1.14 0
17. US-09-841-894A-1	Sequence 10, Application	288	287	287	1.14 0
18. US-08-850-713-11	Sequence 11, Application	272	272	272	1.06 0
19. US-09-071-710-11	Sequence 11, Application	272	270	270	1.04 0
20. US-09-525-397-11	Sequence 11, Application	272	270	270	1.04 0
21. US-09-841-894A-1	Sequence 11, Application	272	270	270	1.04 0
22. US-09-525-397-8	Sequence 8, Application	342	268	328	1.03 0
23. US-09-841-894A-8	Sequence 8, Application	342	268	328	1.03 0
24. US-08-850-713-13	Sequence 13, Application	269	267	267	1.03 0
25. US-08-850-713-3	Sequence 3, Application	268	266	266	1.02 0
26. US-09-071-710-9	Sequence 9, Application	265	265	265	1.02 0
27. US-09-525-397-9	Sequence 9, Application	265	265	265	1.02 0
28. US-08-850-713-10	Sequence 10, Application	265	265	265	1.02 0
29. US-09-841-894A-9	Sequence 9, Application	265	265	265	1.02 0
30. US-09-071-710-1	Sequence 1, Application	258	256	257	0.97 0
31. US-09-525-397-1	Sequence 1, Application	258	256	257	0.97 0
32. US-08-850-713-1	Sequence 1, Application	258	256	257	0.97 0
33. US-09-841-894A-1	Sequence 1, Application	258	256	257	0.97 0
34. US-09-071-710-3	Sequence 3, Application	255	254	254	0.96 0
35. US-09-525-397-3	Sequence 3, Application	255	254	254	0.96 0
36. US-08-850-713-4	Sequence 4, Application	255	254	254	0.96 0
37. US-09-841-894A-3	Sequence 3, Application	255	254	254	0.96 0
38. US-09-071-710-8	Sequence 8, Application	342	251	328	0.94 0
39. US-09-071-710-4	Sequence 4, Application	247	247	247	0.92 0
40. US-09-525-397-4	Sequence 4, Application	247	247	247	0.92 0
41. US-08-850-713-5	Sequence 5, Application	247	247	247	0.92 0
42. US-09-841-894A-4	Sequence 4, Application	247	247	247	0.92 0
43. US-08-850-713-9	Sequence 9, Application	250	218	242	0.76 0
44. US-09-071-710-2	Sequence 2, Application	217	217	217	0.76 0
45. US-09-525-397-2	Sequence 2, Application	217	217	217	0.76 0
46. US-08-850-713-2	Sequence 2, Application	217	217	217	0.76 0


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3030      3040      3050      3060      3070      3080      3090
TTCCCCACCAAGCTCCACAACCCCTGTTTGGAGCTACTCGAGGACCAGAAACACAAGATGCGGTTTCCCAAGCC
TTCCCCACCAAGCTCCACAACCCCTGTTTGGAGCTACTCGAGGACCAGAAACACAAGATGCGGTTTCCCAAGCC
3030      3040      3050      3060      3070      3080      3090
TTTGTCATCTCAGCCGCCAGAGATATCTGTGCTGGGGAATCTCACACAGAACTCAGGAGCACCCCTCTG
TTTGTCATCTCAGCCGCCAGAGATATCTGTGCTGGGGAATCTCACACAGAACTCAGGAGCACCCCTCTG
3100      3110      3120      3130      3140      3150      3160
CTTGAGCTTAAGGGAGGCTTTATCTCTCAGGGGGGTTTAAAGTGCCTTTGCATATATCGCTTATTATTAT
CTTGAGCTTAAGGGAGGCTTTATCTCTCAGGGGGGTTTAAAGTGCCTTTGCATATATCGCTTATTATTAT
3170      3180      3190      3200      3210      3220      3230      3240
TTAGCCGGGTGAATATTTTATCTCTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACAAAAATTAAGGCT
TTAGCCGGGTGAATATTTTATCTCTAAGTGAGCAATCAGAGTATAATGTTTATGGTGACAAAAATTAAGGCT
3250      3260      3270      3280      3290      3300      3310
TTCTTATATGTTTAAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
TTCTTATATGTTTAAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
3320      3330      3340      3350      3360      3370      3380
TTCTTATATGTTTAAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
TTCTTATATGTTTAAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
3390      3400      X
AAAAAATAAAAAAATAAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAA
AAAAAATAAAAAAATAAAAAAATAAAAAA
3390      3400      3410
TTCTTATATGTTTAAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
TTCTTATATGTTTAAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA
3420      3430      3440      3450      3460      3470      3480
TTGATGGCACTCATGACCTTCACGCTGTTTACAGGATTCCTGGGCGAGGGCTGTACAGGCGCTGGCC
TTGATGGCACTCATGACCTTCACGCTGTTTACAGGATTCCTGGGCGAGGGCTGTACAGGCGCTGGCC
1130      1140      1150      1160      1170      1180      1190
AGAGCTGAGCCGGGACCGAGCCCGGACACATATGATGAGGCGTTTCGGATGGGAGCTGGGGCTGTTC
AGAGCTGAGCCGGGACCGAGCCCGGACACATATGATGAGGCGTTTCGGATGGGAGCTGGGGCTGTTC
1200      1210      1220      1230      1240      1250      1260      1270
CTGAGTGCCCATCTCCCTGGTCTCTCTGGTCTATGACCGCGGTGTGCGAGCATTCGGCACTCCGAGCA
CTGAGTGCCCATCTCCCTGGTCTCTCTGGTCTATGACCGCGGTGTGCGAGCATTCGGCACTCCGAGCA
1280      1290      1300      1310      1320      1330      1340
GTGATTTGGCCAGTGCGAGCTTTCCTGTGGCTGCGCGGTGCCACATGCTGCCACAGTGGCGCGTG
GTGATTTGGCCAGTGCGAGCTTTCCTGTGGCTGCGCGGTGCCACATGCTGCCACAGTGGCGCGTG
1350      1360      1370      1380      1390      1400      1410
GTCTATTTGGCCAGTGCGAGCTTTCCTGTGGCTGCGCGGTGCCACATGCTGCCACAGTGGCGCGTG
GTCTATTTGGCCAGTGCGAGCTTTCCTGTGGCTGCGCGGTGCCACATGCTGCCACAGTGGCGCGTG
1420      1430      1440      1450      1460      1470      1480
GTGACAGCTTACCGCCGCTCACCGGTTCCACTTCTAGCCCTGCAGATCTGCCCTACACACTGGCGCTC
GTGACAGCTTACCGCCGCTCACCGGTTCCACTTCTAGCCCTGCAGATCTGCCCTACACACTGGCGCTC
1490      1500      1510      1520      1530      1540      1550
GTGACAGCTTACCGCCGCTCACCGGTTCCACTTCTAGCCCTGCAGATCTGCCCTACACACTGGCGCTC
GTGACAGCTTACCGCCGCTCACCGGTTCCACTTCTAGCCCTGCAGATCTGCCCTACACACTGGCGCTC

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240	250	260	270	280	290	300	310
1490	1500	1510	1520	1530	1540	1550	
CTCTACCACCGGAGAACGGTGTCTCTGCCCAATACCGAGGGACACTGGAGTGTCTAGCAGTAGGAC							
CTCTACACCGGAGAACGGTGTCTCTGCCCAATACCGAGGGACACTGGAGTGTCTAGCAGTAGGAC							
320	330	340	350	360	370	380	
1560	1570	1580	1590	1600	1610	1620	1630
AGCCTGATCACCAGCTTCTCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCTAATAGACACCTGGTCTCGA							
AGCCTGATCACCAGCTTCTCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCTAATAGACACCTGGTCTCGA							
390	400	410	420	430	440	450	
1640	1650	1660	1670	1680	1690	1700	
GGCAGTGGCTCTCCACCTCCACCTCCACCGCGCTCTGGGGGCTCTGCCTGTGATCTCTCCCTAGCTGTGGTG							
GGCAGTGGCTCTCCACCTCCACCGCGCTCTGGGGGCTCTGCCTGTGATCTCTCCCTAGCTGTGGTG							
460	470	480	490	500	510	520	
1710	1720	1730	1740	1750	1760	1770	
GTGGGTGAGCCACCGAGGCCAGGTGTCTCCGGCCGGGGCATCTGCCGTGACCTTCGCCATCTCTGGATAGT							
GTGGGTGAGCCACCGAGGCCAGGTGTCTCCGGCCGGGGCATCTGCCGTGACCTTCGCCATCTCTGGATAGT							
530	540	550	560	570	580	590	
1780	1790	1800	1810	1820	1830	1840	
GCCTTCTGTCTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTTGCCGTGACCTTCGCCATCTCTGGATAGT							
GCCTTCTGTCTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTTGCCGTGACCTTCGCCATCTCTGGATAGT							
600	610	620	630	640	650	660	670
1850	1860	1870	1880	1890	1900	1910	
GCCTATATGGTGTCTCCAGGCTGGGTCTGGTTCGGCATTTACTTTGCTACACAGTAGTATTGTGACAG							
GCCTATATGGTGTCTCCAGGCTGGGTCTGGTTCGGCATTTACTTTGCTACACAGTAGTATTGTGACAG							
680	690	700	710	720	730	740	
1920	1930	1940	1950	1960	1970	1980	
AGCGACTTGGCCAAATACCTACGGTATGAAACCTTCCAGCACATTTGGGGTGGGGCTGCCTCACTGGGTCC							
AGCGACTTGGCCAAATACCTACGGTATGAAACCTTCCAGCACATTTGGGGTGGGGCTGCCTCACTGGGTCC							
750	760	770	780	790	800	810	
2000	2010	2020	2030	2040	2050	2060	
CAGCTCCCGCTCTGTAGCCCATGGGCTGCCGGCTGGCCAGTTTCTGTGTGTCGCAAGTAAT							
CAGCTCCCGCTCTGTAGCCCATGGGCTGCCGGCTGGCCAGTTTCTGTGTGTCGCAAGTAAT							
820	830	840	850	860	870	880	
2070	2080	2090	2100	2110	2120	2130	
TGGCTCTCTGTCACCCCTGCTCTCAGTGGTGTAGCTGCACAGCTGGGGCTGGGCGTCCCTCTCCCT							
TGGCTCTCTGTCACCCCTGCTCTCAGTGGTGTAGCTGCACAGCTGGGGCTGGGCGTCCCTCTCCCT							
890	900	910	920	930	940	950	
2140	2150	2160	2170	2180	2190	2200	
CTCTCCCGCTCTAGGGTGTGCTGACTGGAGGCTTCCAGGGGGTTTCAGTCTCGACTATACAGGGA							
CTCTCCCGCTCTAGGGTGTGCTGACTGGAGGCTTCCAGGGGGTTTCAGTCTCGACTATACAGGGA							
960	970	980	990	1000	1010	1020	
2210	2220	2230	2240	2250	2260	2270	
GCACGAGGGTCCATGCCTAGTAATCGGGGACTCTGCAGTGGATTACCGAGCTCAGGGCTTAACAGCT							
GCACGAGGGTCCATGCCTAGTAATCGGGGACTCTGCAGTGGATTACCGAGCTCAGGGCTTAACAGCT							
1030	1040	1050	1060	1070	1080	1090	1100
2280	2290	2300	2310	2320	2330	2340	2350
GCCTCTAGTTTACACACCTACAGAGGGTTTTGGAGCTGAATAAAGTACAGTACCTGGTTTCCCAT							
GCCTCTAGTTTACACACCTACAGAGGGTTTTGGAGCTGAATAAAGTACAGTACCTGGTTTCCCAT							
1110	1120	1130	1140	1150			

CCCTCTCTGCCATCACAGACACAGAGCATTAAATATTTAACTTTATTTATTTATTTAAACAAGTAGAAGCGCAAT
1400 1410 1420 1430 1440 1450 1460

2640 2650 2660 2670 2680 2690 2700
CCATTGCTAGCTTTTCGTGGTGTCTTAATATTGGTGGAGGTGCGGGATCCCAACAATCAGGTCCCTCT
CCATTGCTAGCTTTTCGTGGTGTCTTAATATTGGTGGAGGTGCGGGATCCCAACAATCAGGTCCCTCT
1470 1480 1490 1500 1510 1520 1530

2710 2720 2730 2740 2750 2760 2770 2780
GAGATAGCTGTGTCATTGGGTGATCATTTGCCAGAACTTTCTTCTCTGGGTCTGGCCCCCAAAATGCCTTA
GAGATAGCTGTGTCATTGGGTGATCATTTGCCAGAACTTTCTTCTCTGGGTCTGGCCCCCAAAATGCCTTA
1540 1550 1560 1570 1580 1590 1600

ACCAGGACCTTGGAAATTTACTTCATCTCCCAAAATGATAATCCAAATGCTTTACCCAAGCTTAGGTGGTGTG
1610 1620 1630 1640 1650 1660 1670 1680
AAGGAAGGTAGAGGTGGGGTTCAGGTCTCAAGGGTTCCTTAACCAACCCCTCTCTCTGGCCCCAGCGGTG
AAGGAAGGTAGAGGTGGGGTTCAGGTCTCAAGGGTTCCTTAACCAACCCCTCTCTCTGGCCCCAGCGGTG
1690 1700 1710 1720 1730 1740 1750

2860 2870 2880 2890 2900 2910 2920
GTTCCTCCCACTTCCACTCCCTCTCTCTAGAGCTGGGTGATGAAGGCATCGCCAAAATTTCCCTCC
GTTCCTCCCACTTCCACTCCCTCTCTCTAGAGCTGGGTGATGAAGGCATCGCCAAAATTTCCCTCC
1760 1770 1780 1790 1800 1810 1820

3000 3010 3020 3030 3040 3050 3060
TACCCCAACTTTCCCTTACCCCAACTTTCCCAACAGCTCCCAACCCCTGTTTGAGCTACTGCAGCAAC
TACCCCAACTTTCCCTTACCCCAACTTTCCCAACAGCTCCCAACCCCTGTTTGAGCTACTGCAGCAAC
1830 1840 1850 1860 1870 1880 1890

3070 3080 3090 3100 3110 3120 3130 3140
AAGAGCAAAAGTCGGTTCACAGCCCTTGTCCATCTCAGCCCCCAGAGTCTTATCTCTCAGGGGGTTTAAGTG
AAGAGCAAAAGTCGGTTCACAGCCCTTGTCCATCTCAGCCCCCAGAGTCTTATCTCTCAGGGGGTTTAAGTG
1900 1910 1920 1930 1940 1950 1960 1970

3150 3160 3170 3180 3190 3200 3210
TCACAGAAACTCAGAGCACCCCTGCTGAGTCAAGGAGGTCTTATCTCTCAGGGGGTTTAAGTG
TCACAGAAACTCAGAGCACCCCTGCTGAGTCAAGGAGGTCTTATCTCTCAGGGGGTTTAAGTG
1970 1980 1990 2000 2010 2020 2030

3220 3230 3240 3250 3260 3270 3280
CGTTTGCATATGTCGCTTATTTATTTAGCGGGTGAATATTTATCTTAAGTGAAGCAATCAGAGTGA
CGTTTGCATATGTCGCTTATTTATTTAGCGGGTGAATATTTATCTTAAGTGAAGCAATCAGAGTGA
2040 2050 2060 2070 2080 2090 2100 2110

3290 3300 3310 3320 3330 3340 3350
AATGTTATGTTGACAAAAATTAAGAGCTTCTTATATGTTTAAAAAATAAAAAAAAAAAAAAAAAAAAA
AATGTTATGTTGACAAAAATTAAGAGCTTCTTATATGTTTAAAAAATAAAAAAAAAAAAAAAAAAAAA
2120 2130 2140 2150 X

3360 3370
AAAAAAAAAAAAAAAAAAAA

4. US-09-030-606-110 (1-3410)
US-09-525-397-16 Sequence 16, Application US/09525397

Initial Score = 1501 Optimized Score = 2144 Significance = 7.67
Residue Identity = 99% Matches = 2149 Mismatches = 1
Conservative Substitutions = 1

4. US-09-030-606-110 (1-3410) Application US/09525397

Initial Score	=	1501	Optimized Score	=	2144	Significance	=	7.67
Residue Identity	=	99%	Matches	=	2149	Mismatches	=	1
Gaps	=	2	Conservative Substitutions	=			=	0

7. US-09-030-606-110 (1-3410)

US-09-525-397-15 Sequence 15, Application US/09525397

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Initial Score      = 1381  Optimized Score = 2129  Significance = 7.03
Residue Identity  = 99%   Matches      = 2139  Mismatches  = 2
Gaps              = 3     Conservative Substitutions = 0
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[illegible]

1140	1150	1160	1170	1180	X 1190	1200
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ACTCATGACCTTCACGCCTTTTACACGGATTCGTGGCGCAGGGGGTGTAACCAAGGCGCTGCCAGAGCTGA
1140 1150 1160 1170 1180 1190 X 1200

1210 1220 1230 1240 1250 1260 1270
GCCGGACCGAGGCCGAGACACTATGATGAGCGCTTCGATGGGACCTGGGGCTGTTCCTCAGTGG
GCCGGACCGAGGCCGAGACACTATGATGAGCGCTTCGATGGGACCTGGGGCTGTTCCTCAGTGG

1280 1290 1300 1310 1320 1330 1340 1350
CGCCATCCCTGCTCTCTCTGGTCATGGACCGCTGGTCAGCGATTGGCACTCCAGCAGCTATT
|||||
CGCCATCCCTGCTCTCTCTGGTCATGGACCGCTGGTCAGCGATTGGCACTCCAGCAGCTATT
|||||
CGCCATCCCTGCTCTCTCTGGTCATGGACCGCTGGTCAGCGATTGGCACTCCAGCAGCTATT
100 110 120 130 140 150 160

1360 1370 1380 1390 1400 1410 1420
GGCAGTGTGGCAGCTTCCCTGTGGTGTCCGCTGCCACATGCCGTGCCACAGTGTGGCCGTGGTGACAGC
|||||
GGCAGTGTGGCAGCTTCCCTGTGGTGTCCGCTGCCACATGCCGTGCCACAGTGTGGCCGTGGTGACAGC
170 180 190 200 210 220 230

1430 1440 1450 1460 1470 1480 1490
TTTACGCGCCCTACCGGGTTACCTTCTCAGCCCTGCAGATCTGCGCTACACACTGGCCTCCCTTACCA
TTTACGCGCCCTACCGGGTTACCTTCTCAGCCCTGCAGATCTGCGCTACACACTGGCCTCCCTTACCA
240 250 260 270 280 290 300 310

1500 1510 1520 1530 1540 1550 1560
CCGGGAGAGCAGGTGTTCTGCCCAATACCGAGGGGACACTGGAGGTCTAGCACTGAGGACAGCCTGAT
CCGGGAGAGCAGGTGTTCTGCCCAATACCGAGGGGACACTGGAGGTCTAGCACTGAGGACAGCCTGAT
CCGGGAGAGCAGGTGTTCTGCCCAATACCGAGGGGACACTGGAGGTCTAGCACTGAGGACAGCCTGAT
CCGGGAGAGCAGGTGTTCTGCCCAATACCGAGGGGACACTGGAGGTCTAGCACTGAGGACAGCCTGAT

1570 1580 1590 1600 1610 1620 1630
GACCAGCTTCCTGCAGGCCCTAAGCTGGAGCTCCCTCCCTAATGGACACCTGGGTCTGGAGGCAGTGG
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|||||
GACCAGCTTCCTGCAGGCCCTAAGCTGGAGCTCCCTCCCTAATGGACACCTGGGTCTGGAGGCAGTGG
390 400 410 420 430 440 450
320 330 340 350 360 370 380

1640 1650 1660 1670 1680 1690 1700 1710
CCTGCTCCACCTCCACCGCGCTCGGGGCGCTCGCTGTGATCTCCGCTACGCTGGTGGGGTGA
CCTGCTCCACCTCCACCGCGCTCGGGGCGCTCGCTGTGATCTCCGCTACGCTGGTGGGGTGA
CCTGCTCCACCTCCACCGCGCTCGGGGCGCTCGCTGTGATCTCCGCTACGCTGGTGGGGTGA
460 470 480 490 500 510 520

[illegible]

1790 1800 1810 1820 1830 1840 1850
GCTGCCAGGTGCCCATCCCTGTTATGGGTCCTATGTCAGCTCAGCCAGTCTGTCACTGCCTATAT
GCTGTCCAGGTGCCCATCCCTGTTATGGGTCCTATGTCAGCTCAGCCAGTCTGTCACTGCCTATAT
GCTGTCCAGGTGCCCATCCCTGTTATGGGTCCTATGTCAGCTCAGCCAGTCTGTCACTGCCTATAT
600 610 620 630 640 650 660 670

[illegible][illegible][illegible][illegible]

890 2150 2160 2170 2180 2190 2200 2210
AGTCTCAGGCGTCCTCGACTGGAGGCCTTCCAAGGGGGTTTAGTGTGCACITATACACGGAGGCCAGAAG

960 AGTCTTAGGCGTCCTGACTGAGCGCTTCCAAAGGGGGTTTCACTGCGACTTATACAGGAGGCCAAGAA
970 980 990 1000 1010 1020 1030
2220 2230 2240 2250 2260 2270 2280
GGCTCCATGCACTGGAAATCGGGGACCTCTCAGGTGGATACCCAGCGTCAGGGTTAAAGCTAGCTCTCTTA

GGCTCCATGCACTGGAATGC - GGGAC^{TCT}CGAGGTCTGCGAT^{TAC}CCAGGCTCAGG^{TTT}AACAGCTAGCCTCCTTA
1040 1050 1060 1070 1080 1090 1100 1110

1110 1120 1130 1140 1150 1160 1170
GTTGAGACACCTTAGAGAGGGTTTTGGGAGCTGAATAAAGTCACTGCTGTTTCCGATCTCTAAGCC
GTTGAGACACCTTAGAGAGGGTTTTGGGAGCTGAATAAAGTCACTGCTGTTTCCGATCTCTAAGCC
GTTGAGACACCTTAGAGAGGGTTTTGGGAGCTGAATAAAGTCACTGCTGTTTCCGATCTCTAAGCC

2360 CCTTAACTGCAGCTTCGGTTTAAATGTTAGCTCTTCATCGGAGGTTCTTAGAGTAAACAC⁺CCTCCATGGGAT
 2370 2380 2390 2400 2410 2420
 2380 CCTTAACTGCAGCTTCGGTTTAAATGTTAGCTCTTCATCGGAGGTTCTTAGAGTAAACAC⁺CCTCCATGGGAT
 2390 2400 2410 2420
 2400 CCTTAACTGCAGCTTCGGTTTAAATGTTAGCTCTTCATCGGAGGTTCTTAGAGTAAACAC⁺CCTCCATGGGAT
 2410 2420
 2420 CCTTAACTGCAGCTTCGGTTTAAATGTTAGCTCTTCATCGGAGGTTCTTAGAGTAAACAC⁺CCTCCATGGGAT

TTGAACATATG - ACTTATTGTAGGGAGAGCTCTGAGGGCAACACACAGAACCGTCCCTCAGCC
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TTGAACATATGAAAGTTTATTGTAGGGGAGAGCTCTGAGGGGCAACACACAGAACCGTCCCTCAGCC

CACAGCACTGTCCTTTTGGCGATCCACC CCCCTTACCTTTATCAGGATGGCCGTGTGGTCCCTTGCT

1320 CACAGCACTGCTTTTGGCTGATCCACCCCTTTACCTTTATCAGAGATGGCCCTGTGTGGTCCCTCTG
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390 TGCCATCACAGAGACACAGGCATTAAATATTTAACTATTTATTTAACAAAGTAGAAGGAATCCATTCT

AGCTTTCGTGTTGGTGCTAATATTGGGTAGGTGGGGATCCCCAACATCAGTCCCTCGAGATAGC
1470 1480 1490 1500 1510 1520 1530

TGGTTCATTGGGCTGCATCATTTGCCAGAAATCTTCTCCTCGGGGTCTGGCCCCCAAAATGCTTAACCCAGA
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TGGTTCATTGGGCTGCATCATTTGCCAGAAATCTTCTCCTCGGGGTCTGGCCCCCAAAATGCTTAACCCAGA
1540 1550 1560 1570 1580 1590 1600

2790	2800	2810	2820	2830	2840	2850	2860
CCCTTGAAATCTACTCATCCCAAATGATAATCCAAATGCTTTACCAAGGTAGGCTGTTCAAGGAAGG							
1610	1620	1630	1640	1650	1660	1670	
CCCTTGAAATCTACTCATCCCAAATGATAATCCAAATGCTTTACCAAGGTAGGCTGTTCAAGGAAGG							
1680	1690	1700	1710	1720	1730	1740	
TAGAGGTTGGGGCTTCAGGCTCAACGGCTTCCTTAACCAACCCCTCTTCTCTTGCCGACGCTGGTTCCTCCC							2930
1750	1760	1770	1780	1790	1800	1810	1820
CACCTTCCCACTCCCTCTACTCTCTAGGACTGGGCTGATGAAGGCACCTGCCCAAATTTCCCTACTACCCCA							
1830	1840	1850	1860	1870	1880	1890	
ACTTTCCCTACCCCAACTTTCCCAACAGCTTCCCAACAGCTCCCAACCCCTGTTGGAGCTACTGCAGGACCAAGACAC							3070
3080	3090	3100	3110	3120	3130	3140	
AAAGTCGGGTTTCCCAAGCCTTGTGCCATCTCAGCCGCCAGAGTATCTGTGCTTGGGGAATCTCACACAG							
1900	1910	1920	1930	1940	1950	1960	
AAAGTCGGGTTTCCCAAGCCTTGTGCCATCTCAGCCGCCAGAGTATCTGTGCTTGGGGAATCTCACACAG							
3150	3160	3170	3180	3190	3200	3210	3220
AAACTCAGGAGCACCCCTGCCTCAGCTAAGGAGGCTTATCTCTCAGGGGGGGTTAAGTCGGCTTGCA							
1970	1980	1990	2000	2010	2020	2030	
AAACTCAGGAGCACCCCTGCCTCAGCTAAGGAGGCTTATCTCTCAGGGGGGGTTAAGTCGGCTTGCA							
3230	3240	3250	3260	3270	3280	3290	
ATAATGTCGCTTATTATTTAGCGGGTGAATATTTATCTAAGTCAGCAATCAGAGTATAATGTGTTA							
2040	2050	2060	2070	2080	2090	2100	
ATAATGTCGCTTATTATTTAGCGGGTGAATATTTATCTAAGTCAGCAATCAGAGTATAATGTGTTA							
3300	3310	3320	3330	3340	3350	3360	
TGCTGACAAATTAAGGCTTCTTATATGTTATAAAAAAATAAAAAAATAAAAAAATAAAAAAATAAAAAA							
2110	2120	2130	2140	X			
TGGTGACAAATTAAGGCTTCTTATATGTTA							
3370							
AAAAAATAAAAAA							

[illegible]

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CGCCATCTCCCTGGTCTTCTCTCTGGTCATGGACGGCTGGTGCACGAGATTGGCAGTCTGCAGACAGTCTATTT
100 110 120 130 140 150 160
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GGCCAGTGTGGCAGTTTCCCTGTGGCTGCGCGGTGCACATGCTCTCCACAGTGTGGCGGTGGTGTGCACAGC
170 180 190 200 210 220 230
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GGCCAGTGTGGCAGTTTCCCTGTGGCTGCGCGGTGCACATGCTCTCCACAGTGTGGCGGTGGTGTGCACAGC
240 250 260 270 280 290 300 310
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TTACAGCGGCCCTCACCGGGTTCCACTTCTACGCCCTGCATCTGCGCTTACACATCGCCCTCCCTCTACCA
1430 1440 1450 1460 1470 1480 1490
TTACAGCGGCCCTCACCGGGTTCCACTTCTACGCCCTGCATCTGCGCTTACACATCGCCCTCCCTCTACCA
1500 1510 1520 1530 1540 1550 1560
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CCGGGAGACAGGTGTTCTCTGCCAAATACCGAGGGGACACTGGAGTGCTAGCACGTGAGCAGACGCTGAT
1570 1580 1590 1600 1610 1620 1630
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GACCAGTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCTTAATGACACACTGGGTGCTGGAGCAGTGG
1640 1650 1660 1670 1680 1690 1700 1710
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CCTGCTCCAGCTCCACCGCGCTGCGGGGCCCTGCCCTGATGTCCTGATGTCCTGACGTGCTGGTGGGTGA
1720 1730 1740 1750 1760 1770 1780
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GCCCACCGAGCCAGGTGTTCCGGCCGGGGCATCTGCTGACCTCGCATCTGGATAGTGCCTTCCT
1790 1800 1810 1820 1830 1840 1850
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GCTGTCCAGGTGGCCCATCCCTGTTATGGGCTCCATGTCCAGCTACGCCAGTGTGCTACTGCGTATAT
1860 1870 1880 1890 1900 1910 1920
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GGTGTCTCCGAGGCTGGGTCTGGTTCGCCATTACTTTGCTACACAGTAGTATTGACAGAGCGACTT
1930 1940 1950 1960 1970 1980 1990
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GGCCAAATACTCAGCGTAGAAATCTCCAGCATTTGGGGTGGAGGCGCTGCTACCTGGCTCCAGCTCCC
2000 2010 2020 2030 2040 2050 2060 2070
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CGCTCTGTTAGCCCATGGGGCTGCGGGCTGCCGCCAGTTCTGTTGCTGCCAAAGTAAATGTGGCTCTC
2080 2090 2100 2110 2120 2130 2140
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TGCTGCCACCCCTGTGCTGAGTGCCTAGCTCCACAGCTGGGGCTGGGGCTGCCCTCTCTCTCTCCCC
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AGTCTCTAGGGCTGCTGACTCGAGGCTCCAGGGGGTTTCAGTCTGGACATTATACAGGAGGCCAAGAG
2220 2230 2240 2250 2260 2270 2280 2290 2300 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400 2410 2420 2430 2440 2450 2460 2470 2480 2490 2500 2510 2520 2530 2540 2550 2560 2570 2580 2590 2600 2610 2620 2630 2640 2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760 2770 2780 2790 2800 2810 2820 2830 2840 2850 2860 2870 2880 2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990 3000 3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120 3130 3140 3150 3160 3170 3180 3190 3200 3210 3220 3230 3240 3250 3260 3270 3280 3290 3300 3310 3320 3330 3340 3350 3360 3370 3380 3390 3400 3410 3420 3430 3440 3450 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650 3660 3670 3680 3690 3700 3710 3720 3730 3740 3750 3760 3770 3780 3790 3800 3810 3820 3830 3840 3850 3860 3870 3880 3890 3900 3910 3920 3930 3940 3950 3960 3970 3980 3990 4000 4010 4020 4030 4040 4050 4060 4070 4080 4090 4100 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200 4210 4220 4230 4240 4250 4260 4270 4280 4290 4300 4310 4320 4330 4340 4350 4360 4370 4380 4390 4400 4410 4420 4430 4440 4450 4460 4470 4480 4490 4500 4510 4520 4530 4540 4550 4560 4570 4580 4590 4600 4610 4620 4630 4640 4650 4660 4670 4680 4690 4700 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 4910 4920 4930 4940 4950 4960 4970 4980 4990 5000 5010 5020 5030 5040 5050 5060 5070 5080 5090 5100 5110 5120 5130 5140 5150 5160 5170 5180 5190 5200 5210 5220 5230 5240 5250 5260 5270 5280 5290 5300 5310 5320 5330 5340 5350 5360 5370 5380 5390 5400 5410 5420 5430 5440 5450 5460 5470 5480 5490 5500 5510 5520 5530 5540 5550 5560 5570 5580 5590 5600 5610 5620 5630 5640 5650 5660 5670 5680 5690 5700 5710 5720 5730 5740 5750 5760 5770 5780 5790 5800 5810 5820 5830 5840 5850 5860 5870 5880 5890 5900 5910 5920 5930 5940 5950 5960 5970 5980 5990 6000 6010 6020 6030 6040 6050 6060 6070 6080 6090 6100 6110 6120 6130 6140 6150 6160 6170 6180 6190 6200 6210 6220 6230 6240 6250 6260 6270 6280 6290 6300 6310 6320 6330 6340 6350 6360 6370 6380 6390 6400 6410 6420 6430 6440 6450 6460 6470 6480 6490 6500 6510 6520 6530 6540 6550 6560 6570 6580 6590 6600 6610 6620 6630 6640 6650 6660 6670 6680 6690 6700 6710 6720 6730 6740 6750 6760 6770 6780 6790 6800 6810 6820 6830 6840 6850 6860 6870 6880 6890 6900 6910 6920 6930 6940 6950 6960 6970 6980 6990 7000 7010 7020 7030 7040 7050 7060 7070 7080 7090 7100 7110 7120 7130 7140 7150 7160 7170 7180 7190 7200 7210 7220 7230 7240 7250 7260 7270 7280 7290 7300 7310 7320 7330 7340 7350 7360 7370 7380 7390 7400 7410 7420 7430 7440 7450 7460 7470 7480 7490 7500 7510 7520 7530 7540 7550 7560 7570 7580 7590 7600 7610 7620 7630 7640 7650 7660 7670 7680 7690 7700 7710 7720 7730 7740 7750 7760 7770 7780 7790 7800 7810 7820 7830 7840 7850 7860 7870 7880 7890 7900 7910 7920 7930 7940 7950 7960 7970 7980 7990 8000 8010 8020 8030 8040 8050 8060 8070 8080 8090 8100 8110 81

2850 2860
TTAGGGTGTGTTGAAGGAAGGTAGAGGGTG

16. US-09-030-606-110 (1-3410)
US-09-525-397-10 Sequence 10, Application US/09525397

Initial score =	287	Optimized Score =	287	Significance =	1.14
Residue Identity =	99%	Matches =	287	Mismatches =	1
Gaps	=	0	Conservative Substitutions	=	0

2490 2500 2510 2520 2530 X 2540 2550
GAACAGGTCCCTCAGCCACACACTGCTTTTGCTGATCCACCCCTCTTACCTTTTATCAGGATGT
|||||
CCTTTACCTTTTATCAGGATGT
X 10 20

2560 2570 2580 2590 2600 2610 2620
GGCCTGTGGTCCCTCTGTCGCCATCACAGACACAGGCAATTAATATTTAACTATTTATTTAACAAAG
|||||
CCTTTACCTTTTATCAGGATGT
X 10 20

2630 2640 2650 2660 2670 2680 2690
TAGAAGGAATCCATTGCTAGCTTTCTGCTGCTCTAAATATTTGGTAGGGTGGGGATCCCCAACAA
|||||
CCTTTACCTTTTATCAGGATGT
X 10 20

2700 2710 2720 2730 2740 2750 2760
TCAGGTCCCTCAGATAGCTGTGCTCATTTGGGCTGATTCATGCCAGAACTCTCTCTCTGGGCTCGCCCC
|||||
CCTTTACCTTTTATCAGGATGT
X 10 20

2770 2780 2790 2800 2810 2820 2830 2840
CAAAATGCCCTAACCCAGGACCTTGGAAATTCATCTATCCCAATGATATTCCAATGCTGTATCCCAAGG
|||||
CCTTTACCTTTTATCAGGATGT
X 10 20

2850 2860
TTAGGGTGTGTTGAAGGAAGGTAGAGGGTG

17. US-09-030-606-110 (1-3410)
US-09-841-894A-1 Sequence 10, Application US/09841894A

Initial score =	287	Optimized Score =	287	Significance =	1.14
Residue Identity =	99%	Matches =	287	Mismatches =	1
Gaps	=	0	Conservative Substitutions	=	0

2490 2500 2510 2520 2530 X 2540 2550
GAACAGGTCCCTCAGCCACACAGCACTGCTTTTGCTGATCCACCCCTCTTACCTTTTATCAGGATGT
|||||
CCTTTACCTTTTATCAGGATGT
X 10 20

2560 2570 2580 2590 2600 2610 2620
GGCCTGTGGTCCCTCTGTCGCCATCACAGACACAGGCAATTAATATTTAACTATTTATTTAACAAAG
|||||
CCTTTACCTTTTATCAGGATGT
X 10 20

2630 2640 2650 2660 2670 2680 2690
TAGAAGGAATCCATTGCTAGCTTTCTGCTGCTCTAAATATTTGGTAGGGTGGGGATCCCCAACAA
|||||
CCTTTACCTTTTATCAGGATGT
X 10 20

2700 2710 2720 2730 2740 2750 2760
TCAGGTCCCTCAGATAGCTGTGCTCATTTGGGCTGATTCATGCCAGAACTCTCTCTCTGGGCTCGCCCC

|||||
TCAGTCCCTGAGATAGCTGCTGATGGCTGATTCGTCAGAAATCTCTCTCTGGGGCTGGCCCC
170 180 190 200 210 220 230
2770 2780 2790 2800 2810 2820 2830 2840
CAAAATGCTTAACCCAGGACCTTGGAAATCTACTATCCCAATGATAATCCAAATGCTGTACCAAGG
|||||
CAAAATGCTTAACCCAGGACCTTGGAAATCTACTATCCCAATGATAAT
240 250 260 270 280 x
2850 2860
TTAGGGTGTTCAGAGAGGTAGAGGGTG

18. US-09-030-606-110 (1-3410)
US-08-850-713-11 Sequence 11, Application US/08850713

Initial Score = 272 Optimized Score = 272 Significance = 1.06
Residue Identity = 100% Matches = 272 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

2610 2620 2630 2640 2650 2660 2670
TTAACTATTATTAAACAAGTAGAGGGAATCCATTGCTAGCTTTCTGTTGGTGTCTAATATTGGG
|||||
GTGTTGGTGTCTAATATTGGG
x 10 20

2680 2690 2700 2710 2720 2730 2740
TAGGGTGGGGATCCCAACATCAGCTGCCCTCAGATAGCTGTGCTATGGGCTGATTCGCCAATCTTT
|||||
TAGGGTGGGGATCCCAACATCAGCTGCCCTCAGATAGCTGTGCTATGGGCTGATTCGCCAATCTTT
30 40 50 60 70 80 90

2750 2760 2770 2780 2790 2800 2810
CTTCTCTGCTGGTCTGGCCCCCAAAATGCTTAACCCAGGACCTTGGAAATCTTACTCATCCCAATGATAA
|||||
CTTCTCTGCTGGTCTGGCCCCCAAAATGCTTAACCCAGGACCTTGGAAATCTTACTCATCCCAATGATAA
100 110 120 130 140 150 160

2820 2830 2840 2850 2860 2870 2880 2890
TTCCAAATGCTTTACCCAGGCTTAGGCTGTGAAGGAAGCTAGAGGTGGGGCTTCAGGTCTCAACGGCTT
|||||
TTCCAAATGCTTTACCCAGGCTTAGGCTGTGAAGGAAGCTAGAGGTGGGGCTTCAGGTCTCAACGGCTT
170 180 190 200 210 220 230

2900 2910 2920 2930 2940 2950 2960
CCCTAACACCCCTCTCTCTGCGCCAGCTGCTTCCGCCCACTTCCACTCCCTCTACTCTCTCTAGGAC
|||||
CCCTAACACCCCTCTCTCTGCGCCAGCTGCTTCCGCCCACTG
240 250 260 270 x

2970
TGGGCTGATGAA

19. US-09-030-606-110 (1-3410)
US-09-071-710-11 Sequence 11, Application US/09071710

Initial Score = 270 Optimized Score = 270 Significance = 1.04
Residue Identity = 99% Matches = 270 Mismatches = 2
Gaps = 0 Conservative Substitutions = 0

2750 2760 2770 2780 2790 2800 2810
CTTCTCTCTGCTGGGCTGGCCCCCAAAATGCTTAACCCAGGACCTTGGAAATCTTACTCATCCCAATGATAA
|||||
AAATCTACTCATCCCAATGATAA
x 10 20

2820 2830 2840 2850 2860 2870 2880
TAATTCCAAATGCTGTACCAAGCTTAGGCTGTGAAGGAAGCTAGAGGTGGGGCTTCAGGTCTCAACGG
|||||
TAATTCCAAATGCTGTACCAAGCTTAGGCTGTGAAGGAAGCTAGAGGTGGGGCTTCAGGTCTCAACGG
30 40 50 60 70 80 90

2890 2900 2910 2920 2930 2940 2950 2960
CTTCCCTAACCAACCCCTCTCTCTTGGCCCAAGCTGGTTCGCCCACTTCCCACTCCCTCTCTCTCTAG
|||||
CTTCCCTAACCAACCCCTCTCTCTTGGCCCAAGCTGGTTCGCCCACTTCCCACTCCCTCTCTCTCTAG
100 110 120 130 140 150 160
2970 2980 2990 3000 3010 3020 3030
GACTGGGCTGATGAAGGCACCTGSCCAAAATTTCCCTACCCCACTTCCCTACCTCCCACTTCCCACT
|||||
GACTGGGCTGATGAAGGCACCTGSCCAAAATTTCCCTACCCCACTTCCCTACCTCCCACTTCCCACT
170 180 190 200 210 220 230
3040 3050 3060 3070 3080 3090 3100
CAGTCCACAAACCCCTGTTGGAGCTACTGTCAGGACCAAGACAAAGTGGGTTTCCCAAGCCTTTGTCCCA
|||||
CAGTCCACAAACCCCTGTTGGAGCTACTGTCAGGACCTTCCCAAGTGGGTTTCCCAAGCCTTTGTCCCA
240 250 260 270 x
3110
TCTCAGGCCCCCA

20. US-09-030-606-110 (1-3410)
US-09-525-397-11 Sequence 11, Application US/09525397

Initial Score = 270 Optimized Score = 270 Significance = 1.04
Residue Identity = 99% Matches = 270 Mismatches = 2
Gaps = 0 Conservative Substitutions = 0

2750 2760 2770 2780 2790 2800 2810
CTTCTCTCTGCTGGGCTGTCGCCCCCAAAATGCTTAACCCAGGACCTTGGAAATCTTACTCATCCCAATGATAA
|||||
AAATCTACTCATCCCAATGATAA
x 10 20

2820 2830 2840 2850 2860 2870 2880
TAATTCCAAATGCTGTACCAAGCTTAGGCTGTGAAGGAAGCTAGAGGTGGGGCTTCAGGTCTCAACGG
|||||
TAATTCCAAATGCTGTACCAAGCTTAGGCTGTGAAGGAAGCTAGAGGTGGGGCTTCAGGTCTCAACGG
30 40 50 60 70 80 90

2890 2900 2910 2920 2930 2940 2950 2960
CTTCCCTAACCAACCCCTCTCTCTTGGCCCAAGCTGGTTCGCCCACTTCCCACTCCCTCTCTCTCTAG
|||||
CTTCCCTAACCAACCCCTCTCTCTTGGCCCAAGCTGGTTCGCCCACTTCCCACTCCCTCTCTCTCTAG
100 110 120 130 140 150 160

2970 2980 2990 3000 3010 3020 3030
GACTGGGCTGATGAAGGCACCTGSCCAAAATTTCCCTACCCCACTTCCCTACCTCCCACTTCCCACT
|||||
GACTGGGCTGATGAAGGCACCTGSCCAAAATTTCCCTACCCCACTTCCCTACCTCCCACTTCCCACT
170 180 190 200 210 220 230
3040 3050 3060 3070 3080 3090 3100
CAGTCCACAAACCCCTGTTGGAGCTACTGTCAGGACCAAGACAAAGTGGGTTTCCCAAGCCTTTGTCCCA
|||||
CAGTCCACAAACCCCTGTTGGAGCTACTGTCAGGACCTTCCCAAGTGGGTTTCCCAAGCCTTTGTCCCA
240 250 260 270 x
3110
TCTCAGGCCCCCA

21. US-09-030-606-110 (1-3410)
US-09-841-894A-1 Sequence 11, Application US/09841894A

Initial Score = 270 Optimized Score = 270 Significance = 1.04
Residue Identity = 99% Matches = 270 Mismatches = 2
Gaps = 0 Conservative Substitutions = 0

2750 2760 2770 2780 2790 2800 2810
CTTCTCTCTGCTGGGCTGTCGCCCCCAAAATGCTTAACCCAGGACCTTGGAAATCTTACTCATCCCAATGATAA
|||||


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|||||
AAATCTACTCATCCCAATGA
X 10 20
2820 2830 2840 2850 2860 2870 2880
TAATCCAAATGCTGTACCCAGGTTAGGGTGTGAAGGAGGTAGAGGTGGGGCTTTCAGGTCTCAACGG
|||||
TAATCCAAATGCTGTACCCAGGTTAGGGTGTGAAGGAGGTAGAGGTGGGGCTTTCAGGTCTCAACGG
30 40 50 60 70 80 90
2890 2900 2910 2920 2930 2940 2950 2960
CTTCCCTAACCAACCCCTCTCTCTTGGCCAGCCTGGTTCCTCCCACTTCCACTCCCTCTACTCTCTCTAG
|||||
CTTCCCTAACCAACCCCTCTCTCTTGGCCAGCCTGGTTCCTCCCACTTCCACTCCCTCTACTCTCTCTAG
100 110 120 130 140 150 160
2970 2980 2990 3000 3010 3020 3030
GACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCTACCCCACTTCCCTACCCCACTTCCCTAC
|||||
GACTGGGCTGATGAAGGCACTGCCCAAAATTTCCCTACCCCACTTTCCTACCCCACTTCCCTAC
170 180 190 200 210 220 230
3040 3050 3060 3070 3080 3090 3100
CAGCTCCACAAACCCCTGTGTGGAGCTACTGCGAGGACCAAGGACAAAGTGCCTTCCCAAGCCTTTGFCGA
|||||
CAGCTCCACAAACCCCTGTGTGGAGCTACTGCGAGGACCAAGGACCAAGTGCCTTCCCAAGCCTTTGFCGA
240 250 260 270 X
TCTCAGCCCCCA
3110

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22. US-09-030-606-110 (1-3410)
US-09-525-397-8 Sequence 8, Application US/09525397

Initial Score = 268 Optimized Score = 328 Significance = 1.03
Residue Identity = 97% Matches = 333 Mismatches = 7
Gaps = 2 Conservative Substitutions = 0

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2160 2170 2180 2190 2200 2210 2220
CCTGACTGGAGGCCCTTCCAGGGGTTTCAGTCTGGACTTATACAGGGAGGCGAGAGGCGCTCCATGCACTG
|||||
GCCAAGAGGCTCCATGCACTG
X 10 20
2230 2240 2250 2260 2270 2280 2290 2300
GAATCGGGGACTCTGCAAGTGGATTACCCAGGCTCAGGTTTACAGCTAGCCTCTCTAGTTGAGACACCT
|||||
GAATCGGGGACTCTGCAAGTGGATTACCCAGGCTCAGGTTTACAGCTAGCCTCTCTAGTTGAGACACCT
30 40 50 60 70 80 90
2310 2320 2330 2340 2350 2360 2370
AGAGAGGGTTTTGGGAGCTGAATAAGCTCAGTCACCTGGTTCCTCCATCTCTAAGCCCTTAACTCAGC
|||||
AGAGAGGGTTTTGGGAGCTGAATAAGCTCAGTCACCTGGTTCCTCCATCTCTAAGCCCTTAACTCAGC
100 110 120 130 140 150 160
2380 2390 2400 2410 2420 2430 2440
TTCTGTTAATGAGTCTGTGATGGAGTTTCTAGGATGAACACTCTCTCCATGGGATTTGAACATATG--A
|||||
TTCTGTTAATGAGTCTGTGATGGAGTTTCTAGGATGAACACTCTCTCCATGGGATTTGAACATATG--A
170 180 190 200 210 220 230
2450 2460 2470 2480 2490 2500 2510
CTTATTGTAGGGAGAGTCTCTGAGGGCAACACACAAAGAACAGGTCCCTCAGGCCACAGCACTGTCTT
|||||
CTTATTGTAGGGAGAGTCTCTGAGGGCAACACACAAAGAACAGGTCCCTCAGGCCACAGCACTGTCTT
240 250 260 270 280 290 300 310
2520 2530 2540 2550 2560 2570 2580
TTTGTGATCCACCCCTCTTACCTTTTATCAGGATGTGGCTTGTGCTCTTCTGTGCTATCAGAGAGA
|||||
TTTGTGATCCACCCCTCTTACCTTTTATCA

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320 330 340 X
2590
CACAGGCATT

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23. US-09-030-606-110 (1-3410)
US-09-841-894A-8 Sequence 8, Application US/09841894A

Initial Score = 268 Optimized Score = 328 Significance = 1.03
Residue Identity = 97% Matches = 333 Mismatches = 7
Gaps = 2 Conservative Substitutions = 0

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2160 2170 2180 2190 2200 2210 2220
CCTGACTGGAGGCCCTTCCAGGGGTTTTCAGTCTGGACTTATACAGGAGGCCAAGAGGCTTCCATGCACTG
|||||
GCCAAGAGGCTCCATGCACTG
X 10 20
2230 2240 2250 2260 2270 2280 2290 2300
GAATCGGGGACTCTGCAAGTGGATTACCCAGGCTCAGGTTTAAACAGCTAGCCTCTCTAGTTGAGACACCT
|||||
GAATCGGGGACTCTGCAAGTGGATTACCCAGGCTCAGGTTTAAACAGCTAGCCTCTCTAGTTGAGACACCT
30 40 50 60 70 80 90
2310 2320 2330 2340 2350 2360 2370
AGAGAGGGTTTTGGGAGCTGAATAAGCTCAGTCACCTGGTTCCTCCATCTCTAAGCCCTTAACTCAGC
|||||
AGAGAGGGTTTTGGGAGCTGAATAAGCTCAGTCACCTGGTTCCTCCATCTCTAAGCCCTTAACTCAGC
100 110 120 130 140 150 160
2380 2390 2400 2410 2420 2430 2440
TTCTGTTAATGAGTCTGTGATGGAGTTTCTAGGATGAACACTCTCTCCATGGGATTTGAACATATG--A
|||||
TTCTGTTAATGAGTCTGTGATGGAGTTTCTAGGATGAACACTCTCTCCATGGGATTTGAACATATGAA
170 180 190 200 210 220 230
2450 2460 2470 2480 2490 2500 2510
CTTATTGTAGGGAGAGTCTCTGAGGGCAACACACAAAGAACAGGTCCCTCAGGCCACAGCACTGTCTT
|||||
CTTATTGTAGGGAGAGTCTCTGAGGGCAACACACAAAGAACAGGTCCCTCAGGCCACAGCACTGTCTT
240 250 260 270 280 290 300 310
2520 2530 2540 2550 2560 2570 2580
TTTGTGATCCACCCCTCTTACCTTTTATCAGGATGTGGCTTGTGCTCTTCTGTGCTATCAGAGAGA
|||||
TTTGTGATCCACCCCTCTTACCTTTTATCA

```

24. US-09-030-606-110 (1-3410)
US-08-850-713-13 Sequence 13, Application US/08850713

Initial Score = 267 Optimized Score = 267 Significance = 1.03
Residue Identity = 99% Matches = 267 Mismatches = 2
Gaps = 0 Conservative Substitutions = 0

```

2850 2860 2870 2880 2890 2900 2910 2920
GTTGAAGGAAGGTAGAGGTGGGGCTTTCAGGTCTCAACGGCTTCCCTAACCCCTCTTCTCTTGGCCAG
|||||
CACCCTCTTCTCTTGGCCAG
X 10 20
2930 2940 2950 2960 2970 2980 2990
CCTGGTTCCTCCCACTTCCACTCCCTCTACTCTCTAGGACTGGGCTGATGAAGCACTGCCCAAAATTT
|||||
CCTGGTTCCTCCCACTTCCACTCCCTCTACTCTCTAGGACTGGGCTGATGAAGCACTGCCCAAAATTT
30 40 50 60 70 80 90
3000 3010 3020 3030 3040 3050 3060

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CCCTACCCCAACTTTCCCTACCCCAACTTTCCCAACAGCTCCCAACCCCTGTTTGAGACTACTGCAG
|||||
CCCTACCCCAACTTTCCCTACCCCAACTTTCCCAACAGCTCCCAACCCCTGTTTGAGACTACTGCAG
100 110 120 130 140 150 160

3070 3080 3090 3100 3110 3120 3130
GACCAAGACACAAGTGGCGGTTTCCCAAGCTTTGCCATTCAGCCCCCAGAGTATATCTGTGCTTGGGG
|||||
GACCAAGACACAAGTGGCGGTTTCCCAAGCTTTGCCATTCAGCCCCCAGAGTATATCTGTGCTTGGGG
170 180 190 200 210 220 230

3140 3150 3160 3170 3180 3190 3200
AATCTACAGAAACTCAGAGACACCCCTGCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGGTTAA
|||||
AATCTACAGAAACTCAGAGACACCCCTGCTGAGCTAAGGGAGGTCTTATCTCTCAGGGGGGGTTAA
240 250 260 X

3210
GTGCCGTTT

25. US-09-030-606-110 (1-3410)
US-08-850-713-3 Sequence 3, Application US/08850713

Initial Score = 266 Optimized Score = 266 Significance = 1.02
Residue Identity = 9% Matches = 266 Mismatches = 2
Gaps = 0 Conservative Substitutions = 0

1210 1220 1230 1240 1250 1260 1270
GCCGGGACCGAGCCCGGAGACACTATGATGAAGCGTTCGGATGGGAGCCGCGGGCTGTTCTCTGCAGTG
|||||
GCCGGGACCGAGCCCGGAGACACTATGATGAAGCGTTCGGATGGGAGCCGCGGGCTGTTCTCTGCAGTG
X 10 20

1280 1290 1300 1310 1320 1330 1340 1350
CGCCATCTCCCTGCTCTCTCTGTCATGAGCGCGCTGGTGCAGGATTCGCACTCGAGCAGTCTATTT
|||||
CGCCATCTCCCTGCTCTCTCTGTCATGAGCGCGCTGGTGCAGGATTCGCACTCGAGCAGTCTATTT
30 40 50 60 70 80 90

1360 1370 1380 1390 1400 1410 1420
GGCCAGTGGCAGCTTTCCCTGTGGCTGCGGTCACATGCTGTCACAGTGGCGGCTGGTGCACAGC
|||||
GGCCAGTGGCAGCTTTCCCTGTGGCTGCGGTCACATGCTGTCACAGTGGCGGCTGGTGCACAGC
100 110 120 130 140 150 160

1430 1440 1450 1460 1470 1480 1490
TTCAGCCGCTTCCACCGGTTCACTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCCTCCTACCA
|||||
TTCAGCCGCTTCCACCGGTTCACTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCCTCCTACCA
170 180 190 200 210 220 230

1500 1510 1520 X 1530 1540 1550 1560
CCGGGAGAACAGGTGTTCTTCCCAATACCGAGGGGACACTGGAGTGTCTAGCAGTGAGGACAGCCTGAT
|||||
CCGGGAGAACAGGTGTTCTTCCCAATACCGAGGGGACACTGGAGTGTCTAGCAGTGAGGACAGCCTGAT
240 250 260 X

1570
GACCACT

26. US-09-030-606-110 (1-3410)
US-09-071-710-9 Sequence 9, Application US/09071710

Initial Score = 265 Optimized Score = 265 Significance = 1.02
Residue Identity = 100% Matches = 265 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

2410 2420 2430 2440 2450 X 2460 2470
TCTAGGATGAACACTCTCTCCATCGGATTTGAACATATGATCTTATTTGAGGGGAGAGTCTCAGGGGCA
|||||
TCTAGGATGAACACTCTCTCCATCGGATTTGAACATATGATCTTATTTGAGGGGAGAGTCTCAGGGGCA
GGGGAAGAGTCTCAGGGGCA

2480 2490 2500 2510 2520 2530 2540
CACACAGAACCAGTCCCTCAGCCACAGCACTGCTTTTCTGCTGATCCACCCCTCTTACCTTTATC
|||||
CACACAGAACCAGTCCCTCAGCCACAGCACTGCTTTTCTGCTGATCCACCCCTCTTACCTTTATC
30 40 50 60 70 80 90

2550 2560 2570 2580 2590 2600 2610
AGATGTGGCTGTTGCTCTCTGTTGCCATCAGAGACAGGATTTAAATATTTAACTTATTTATTT
|||||
AGATGTGGCTGTTGCTCTCTGTTGCCATCAGAGACAGGATTTAAATATTTAACTTATTTATTT
100 110 120 130 140 150 160

2620 2630 2640 2650 2660 2670 2680 2690
AACAAAGTAGAAGGAATCCATTCCTAGCTTTCTGTTGGTCTCTAAATTTGGGTAGGTGGGGATCC
|||||
AACAAAGTAGAAGGAATCCATTCCTAGCTTTCTGTTGGTCTCTAAATTTGGGTAGGTGGGGATCC
170 180 190 200 210 220 230

2700 2710 2720 2730 2740 2750 2760
CCAAATCAGTCCCTGAGATAGCTGGTCAATTGGGCTGATCATTTGCCAGATCTTCTTCTCCTGGGTCT
|||||
CCAAATCAGTCCCTGAGATAGCTGGTCAATTGGGCTGATCATTTGCCAGATCTTCTTCTCCTGGGTCT
240 250 260 X

GGCCC

27. US-09-030-606-110 (1-3410)
US-09-525-397-9 Sequence 9, Application US/09525397

Initial Score = 265 Optimized Score = 265 Significance = 1.02
Residue Identity = 100% Matches = 265 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

2410 2420 2430 2440 2450 X 2460 2470
TCTAGGATGAACACTCTCTCCATCGGATTTGAACATATGACTTATTTGAGGGGAGAGTCTCAGGGGCAA
|||||
TCTAGGATGAACACTCTCTCCATCGGATTTGAACATATGACTTATTTGAGGGGAGAGTCTCAGGGGCAA
GGGGAAGAGTCTCAGGGGCAA
X 10 20

2480 2490 2500 2510 2520 2530 2540
CACACAGAACCAGTCCCTCAGCCACAGCACTGCTTTTCTGCTGATCCACCCCTCTTACCTTTATC
|||||
CACACAGAACCAGTCCCTCAGCCACAGCACTGCTTTTCTGCTGATCCACCCCTCTTACCTTTATC
30 40 50 60 70 80 90

2550 2560 2570 2580 2590 2600 2610
AGATGTGGCTGTTGCTCTCTGTTGCCATCAGAGACAGGATTTAAATATTTAACTTATTTATTT
|||||
AGATGTGGCTGTTGCTCTCTGTTGCCATCAGAGACAGGATTTAAATATTTAACTTATTTATTT
100 110 120 130 140 150 160

2620 2630 2640 2650 2660 2670 2680 2690
AACAAAGTAGAAGGAATCCATTCCTAGCTTTCTGTTGGTCTCTAAATTTGGGTAGGTGGGGATCC
|||||
AACAAAGTAGAAGGAATCCATTCCTAGCTTTCTGTTGGTCTCTAAATTTGGGTAGGTGGGGATCC
170 180 190 200 210 220 230

2700 2710 2720 2730 2740 2750 2760
CCAAATCAGTCCCTGAGATAGCTGGTCAATTGGGCTGATCATTTGCCAGATCTTCTTCTCCTGGGTCT
|||||
CCAAATCAGTCCCTGAGATAGCTGGTCAATTGGGCTGATCATTTGCCAGATCTTCTTCTCCTGGGTCT
240 250 260 X

GGCCC

28. US-09-030-606-110 (1-3410)
US-08-850-713-10 Sequence 10, Application US/08850713

Initial Score = 265 Optimized Score = 265 Significance = 1.02
Residue Identity = 100% Matches = 265 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

2410 2420 2430 2440 2450 2460 2470
TCTAGATGAACACTCCTCCATGGATTGACATATGACTTATTTGAGGAGAGACTCTGAGGGCAA
|||||
GGGGAAGAGTCTCTGAGGGCAA
X 10 20

2480 2490 2500 2510 2520 2530 2540
CACAAAGAACAGTCCCTCAGCCACAGACACTGTCTTTTGTGATGACACCCCTCTTACCTTTATC
|||||
CACAAAGAACAGTCCCTCAGCCACAGACACTGTCTTTTGTGATGACACCCCTCTTACCTTTATC
30 40 50 60 70 80 90

2550 2560 2570 2580 2590 2600 2610
AGGATGTGCCCTGTGGTCTCTCTGTCATGACAGACAGGCAATTTAAATATTAACTTATTATTT
|||||
AGGATGTGCCCTGTGGTCTCTCTGTCATGACAGACAGGCAATTTAAATATTAACTTATTATTT
100 110 120 130 140 150 160

2620 2630 2640 2650 2660 2670 2680 2690
AACAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTGCTCTAATATTGGGTAGGTGGGGATCC
|||||
AACAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTGCTCTAATATTGGGTAGGTGGGGATCC
170 180 190 200 210 220 230

2700 2710 2720 2730 2740 2750 2760
CCAACAATCAGTCCCTCAGATAGCTGTGTCATGTTGGCTGATCATTTGCCAGAATCTTCTCTCGGGGTCT
|||||
CCAACAATCAGTCCCTCAGATAGCT
240 250 260 X

GGCCC

29. US-09-030-606-110 (1-3410)
US-09-841-894A-9 Sequence 9, Application US/09841894A
Initial Score = 265 Optimized Score = 265 Significance = 1.02
Residue Identity = 100% Matches = 265 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

2410 2420 2430 2440 2450 2460 2470
TCTAGATGAACACTCCTCCATGGATTGACATATGACTTATTTGAGGAGAGACTCTCTGAGGGCAA
|||||
GGGGAAGAGTCTCTGAGGGCAA
X 10 20

2480 2490 2500 2510 2520 2530 2540
CACAAAGAACAGTCCCTCAGCCACAGACACTGTCTTTTGTGATGACACCCCTCTTACCTTTATC
|||||
CACAAAGAACAGTCCCTCAGCCACAGACACTGTCTTTTGTGATGACACCCCTCTTACCTTTATC
30 40 50 60 70 80 90

2550 2560 2570 2580 2590 2600 2610
AGGATGTGCCCTGTGGTCTCTCTGTCATGACAGACAGGCAATTTAAATATTAACTTATTATTT
|||||
AGGATGTGCCCTGTGGTCTCTCTGTCATGACAGACAGGCAATTTAAATATTAACTTATTATTT
100 110 120 130 140 150 160

2620 2630 2640 2650 2660 2670 2680 2690
AACAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTGCTCTAATATTGGGTAGGTGGGGATCC
|||||
AACAAGTAGAAGGGAATCCATTGCTAGCTTTTCTGTGTGCTCTAATATTGGGTAGGTGGGGATCC
170 180 190 200 210 220 230

2700 2710 2720 2730 2740 2750 2760
CCAACAATCAGTCCCTCAGATAGCTGTGTCATGTTGGCTGATCATTTGCCAGAATCTTCTCTCGGGGTCT
|||||
CCAACAATCAGTCCCTCAGATAGCT
240 250 260 X

GGCCC

30. US-09-030-606-110 (1-3410)
US-09-071-710-1 Sequence 1, Application US/09071710
Initial Score = 256 Optimized Score = 257 Significance = 0.97
Residue Identity = 99% Matches = 257 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

1130 1140 1150 1160 1170 1180 1190
TGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGCGAGGGCTGTACACAGGCGTGC
|||||
GGGGCTGTACACAGGCGTGC
X 10 20

1200 1210 1220 1230 1240 1250 1260 1270
AGAGCTGAGCCGGGCAACCGAGCCCGGAGACACTATGATGAAGCGTTTCGGATGGGCACTGGGGCTGTTTC
|||||
AGAGCTGAGCCGGGCAACCGAGCCCGGAGACACTATGATGAAGCGTTTCGGATGGGCACTGGGGCTGTTTC
30 40 50 60 70 80 90

1280 1290 1300 1310 1320 1330 1340
CTGCAGTGGCCCATCTCCCTGCTCTCTCTGTCATGACCGGCTGTGCAGCGATTTCGGCACTCGAGCA
|||||
CTGCAGTGGCCCATCTCCCTGCTCTCTCTGTCATGACCGGCTGTGCAGCGATTTCGGCACTCGAGCA
100 110 120 130 140 150 160

1350 1360 1370 1380 1390 1400 1410
GTCTATTGGCCAGTGTGGCAGCTTTCCCTGTGCTGCGGTGCCACATGCTGTCCCACAGTGTGGCGCTG
|||||
GTCTATTGGCCAGTGTGGCAGCTTTCCCTGTGCTGCGGTGCCACATGCTGTCCCACAGTGTGGCGCTG
170 180 190 200 210 220 230

1420 1430 1440 1450 1460 1470 1480
GTGCAGCTTCAGCGCCCTCACCGGTTACCTTCTCAGCCCTTSCAGATCCTGCGCTTACACACTGGCCT
|||||
GTGCAGCTTCAGCGCCCT
240 250 X

31. US-09-030-606-110 (1-3410)
US-09-525-397-1 Sequence 1, Application US/09525397
Initial Score = 256 Optimized Score = 257 Significance = 0.97
Residue Identity = 99% Matches = 257 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

1130 1140 1150 1160 1170 1180 1190
TGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGCGAGGGCTGTACACAGGCGTGC
|||||
GGGGCTGTACACAGGCGTGC
X 10 20

1200 1210 1220 1230 1240 1250 1260 1270
AGAGCTGAGCCGGGCAACCGAGCCCGGAGACACTATGATGAAGCGTTTCGGATGGGCACTGGGGCTGTTTC
|||||
AGAGCTGAGCCGGGCAACCGAGCCCGGAGACACTATGATGAAGCGTTTCGGATGGGCACTGGGGCTGTTTC
30 40 50 60 70 80 90

1280 1290 1300 1310 1320 1330 1340
CTGCAGTGGCCCATCTCCCTGCTCTCTCTGTCATGACCGGCTGTGCAGCGATTTCGGCACTCGAGCA
|||||
CTGCAGTGGCCCATCTCCCTGCTCTCTCTGTCATGACCGGCTGTGCAGCGATTTCGGCACTCGAGCA
100 110 120 130 140 150 160

1350 1360 1370 1380 1390 1400 1410
GTCTATTGGCCAGTGTGGCAGCTTTCCCTGTGCTGCGGTGCCACATGCTGTCCCACAGTGTGGCGCTG
|||||
GTCTATTGGCCAGTGTGGCAGCTTTCCCTGTGCTGCGGTGCCACATGCTGTCCCACAGTGTGGCGCTG
170 180 190 200 210 220 230

CCAACAATCAGTCCCTCAGATAGCT
240 250 260 X

GGCCC

GTCTATTGGCCAGTGTGGCAGCTTTCCCTGTCGGTGTCCAGATGCTTCCACAGTGTGCCCGTG
170 180 190 200 210 220 230
1420 1430 X 1440 1450 1460 1470 1480
GTGACAGCTTCAGCCGCCCTCACCAGGTTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCT
|||||
GTGACAGCTTCAGCCGCCCTT X
240 250

32. US-09-030-606-110 (1-3410)
US-08-850-713-1 Sequence 1, Application US/08850713

Initial Score = 256 Optimized Score = 257 Significance = 0.97
Residue Identity = 99% Matches = 257 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

1130 1140 1150 1160 1170 1180 1190
TGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGCGAGGGCTGTACACAGGGGTGCC
|||||
GGGGCTGTACACAGGGGTGCC
X
20

1200 1210 1220 1230 1240 1250 1260 1270
AGAGCTGAGCCGGGACCGAGGCCGAGACACTATGATGAAGCGTTCGGATGGCGAGCCTGGGGCTGTC
|||||
AGAGCTGAGCCGGGACCGAGGCCGAGACACTATGATGAAGCGTTCGGATGGCGAGCCTGGGGCTGTC
30 40 50 60 70 80 90
1280 1290 1300 1310 1320 1330 1340
CTCAGTGGCCCATCTCCCTGGTCTCTCTGGTATGAGCCGGCTGGTGGCAGCTTGGCACTCGAGCA
|||||
CTCAGTGGCCCATCTCCCTGGTCTCTCTGGTATGAGCCGGCTGGTGGCAGCTTGGCACTCGAGCA
100 110 120 130 140 150 160

1350 1360 1370 1380 1390 1400 1410
GTCTATTGGCCAGTGTGGCAGCTTTCCCTGTCGGTGTCCAGATGCTTCCACAGTGTGCCCGTG
|||||
GTCTATTGGCCAGTGTGGCAGCTTTCCCTGTCGGTGTCCAGATGCTTCCACAGTGTGCCCGTG
170 180 190 200 210 220 230
1420 1430 X 1440 1450 1460 1470 1480
GTGACAGCTTCAGCCGCCCTCACCAGGTTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCCT
|||||
GTGACAGCTTCAGCCGCCCTT X
240 250

33. US-09-030-606-110 (1-3410)
US-09-841-894A-1 Sequence 1, Application US/09841894A

Initial Score = 256 Optimized Score = 257 Significance = 0.97
Residue Identity = 99% Matches = 257 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

1130 1140 1150 1160 1170 1180 1190
TGGATGGCACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGCGAGGGCTGTACACAGGGGTGCC
|||||
GGGGCTGTACACAGGGGTGCC
X
20

1200 1210 1220 1230 1240 1250 1260 1270
AGAGCTGAGCCGGGACCGAGGCCGAGACACTATGATGAAGCGTTCGGATGGCGAGCCTGGGGCTGTC
|||||
AGAGCTGAGCCGGGACCGAGGCCGAGACACTATGATGAAGCGTTCGGATGGCGAGCCTGGGGCTGTC
30 40 50 60 70 80 90
1280 1290 1300 1310 1320 1330 1340
CTCAGTGGCCCATCTCCCTGGTCTCTCTGGTATGAGCCGGCTGGTGGCAGCTTGGCACTCGAGCA
|||||
CTCAGTGGCCCATCTCCCTGGTCTCTCTGGTATGAGCCGGCTGGTGGCAGCTTGGCACTCGAGCA
100 110 120 130 140 150 160

1350 1360 1370 1380 1390 1400 1410
GTCTATTGGCCAGTGTGGCAGCTTTCCCTGTCGGTGTCCAGATGCTTCCACAGTGTGCCCGTG
|||||
GTCTATTGGCCAGTGTGGCAGCTTTCCCTGTCGGTGTCCAGATGCTTCCACAGTGTGCCCGTG
170 180 190 200 210 220 230
1420 1430 X 1440 1450 1460 1470 1480
GTGACAGCTTCAGCCGCCCTCACCAGGTTTACCTTCTCAGCCCTGCAGATCCTGCCCTACACTGGCCT
|||||
GTGACAGCTTCAGCCGCCCTT X
240 250

34. US-09-030-606-110 (1-3410)
US-09-071-710-3 Sequence 3, Application US/09071710

Initial Score = 254 Optimized Score = 254 Significance = 0.96
Residue Identity = 99% Matches = 254 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

1370 1380 1390 1400 1410 1420 1430
TTCCTGTGGCTGCCGTGCCACATGCTGTCCACAGTGTGGCCGTGTGACAGCTTCAGCCGCCCTCACC
|||||
GACAGCTTCAGCCGCCCTCACC
X
20

1440 1450 1460 1470 1480 1490 1500 1510
GGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCTTCTACACCGGGAGAGCAGGTG
|||||
GGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCTTCTACACCGGGAGAGCAGGTG
30 40 50 60 70 80 90
1520 1530 1540 1550 1560 1570 1580
TTCCTGCCCAATACCGGGGACACTGGAGTGTCTAGCAGTGGAGACAGCTGATCACCAGCTTCTCGCA
|||||
TTCCTGCCCAATACCGGGGACACTGGAGTGTCTAGCAGTGGAGACAGCTGATCACCAGCTTCTCGCA
100 110 120 130 140 150 160

1590 1600 1610 1620 1630 1640 1650
GGCCCTAAGCTTGAGCTTCCCTTAATGGACACGTGGTGTGGAGCAGTGGCTCTGCCACCTCGCA
|||||
GGCCCTAAGCTTGAGCTTCCCTTAATGGACACGTGGTGTGGAGCAGTGGCTCTGCCACCTCGCA
170 180 190 200 210 220 230
1660 1670 1680 1690 1700 1710 1720
CCCGGCTCTGCGGGCTCTGCTGTGATGTCTCCGTAGCTGTGGTGTGGTGTGAGCCACCGAGG
|||||
CCCGGCTCTGCGGGCT X
240 250

35. US-09-030-606-110 (1-3410)
US-09-525-397-3 Sequence 3, Application US/09525397

Initial Score = 254 Optimized Score = 254 Significance = 0.96
Residue Identity = 99% Matches = 254 Mismatches = 1
Gaps = 0 Conservative Substitutions = 0

1370 1380 1390 1400 1410 1420 1430
TTCCTGTGGCTGCCGTGCCACATGCTGTCCACAGTGTGGCCGTGTGACAGCTTCAGCCGCCCTCACC
|||||
GACAGCTTCAGCCGCCCTCACC
X
20

1440 1450 1460 1470 1480 1490 1500 1510
GGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCTTCTACACCGGGAGAGCAGGTG
|||||
GGGTTCACCTTCTCAGCCCTGCAGATCCTGCCCTACACACTGGCTTCTACACCGGGAGAGCAGGTG
30 40 50 60 70 80 90
1520 1530 1540 1550 1560 1570 1580
TTCCTGCCCAATACCGGGGACACTGGAGTGTAGCAGTGGAGACAGCTGATGACAGCTTCTCGCA
|||||

TTCTGCCCCAAATACCGAGGACACTGGAGGTGCTAGCAGTGAAGACAGCCTGATGACCACTTCCTGCGCA
 100 110 120 130 140 150 160
 1590 1600 1610 1620 1630 1640 1650
 GGCCTTAAGCTGGAGTCCCTTCCTTAATGACACAGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCA
 170 180 190 200 210 220 230
 GGCCTTAAGCTGGAGTCCCTTCCTTAATGACACAGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCA
 1660 1670 1680 1690 1700 1710 1720
 CCGGCTCTGGGGGCTCTCCCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCACCGAGG
 170 180 190 200 210 220 230
 CCGGCTCTGGGGGCTCTCCCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCACCGAGG
 240 250 X

36. US-09-030-606-110 (1-3410)
 US-08-850-713-4 Sequence 4, Application US/08850713

Initial Score = 254 Optimized Score = 254 Significance = 0.96
 Residue Identity = 99% Matches = 254 Mismatches = 1
 Gaps = 0 Conservative Substitutions = 0

1370 1380 1390 1400 1410 1420 1430
 TTCCCTGTGGCTGCCGGTCCACATGCTGCTCCACAGTGGCCGTGACAGCTTCAGCCGCGCCCTCACC
 1440 1450 1460 1470 1480 1490 1500 1510
 GGTTCACCTTCTCAGCCTTCAGATCTTCCTTACACTGGCTTCCCTCTACACCGGGAGAGCAGGTG
 1520 1530 1540 1550 1560 1570 1580
 TTCTGCCCCAAATACCGAGGACACTGGAGGTGCTAGCAGTGAAGACAGCCTGATGACCACTTCCTGCGCA
 160 170 180 190 200 210 220 230
 GGCCTTAAGCTGGAGTCCCTTCCTTAATGACACAGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCA
 1660 1670 1680 1690 1700 1710 1720
 CCGGCTCTGGGGGCTCTCCCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCACCGAGG
 170 180 190 200 210 220 230
 CCGGCTCTGGGGGCTCTCCCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCACCGAGG
 240 250 X

37. US-09-030-606-110 (1-3410)
 US-09-841-894A-3 Sequence 3, Application US/09841894A

Initial Score = 254 Optimized Score = 254 Significance = 0.96
 Residue Identity = 99% Matches = 254 Mismatches = 1
 Gaps = 0 Conservative Substitutions = 0

1370 1380 1390 1400 1410 1420 1430
 TTCCCTGTGGCTGCCGGTCCACATGCTGCTCCACAGTGGCCGTGACAGCTTCAGCCGCGCCCTCACC
 1440 1450 1460 1470 1480 1490 1500 1510
 GGTTCACCTTCTCAGCCTTCAGATCTTCCTTACACTGGCTTCCCTCTACACCGGGAGAGCAGGTG
 1520 1530 1540 1550 1560 1570 1580
 TTCTGCCCCAAATACCGAGGACACTGGAGGTGCTAGCAGTGAAGACAGCCTGATGACCACTTCCTGCGCA
 160 170 180 190 200 210 220 230
 GGCCTTAAGCTGGAGTCCCTTCCTTAATGACACAGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCA
 1660 1670 1680 1690 1700 1710 1720
 CCGGCTCTGGGGGCTCTCCCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCACCGAGG
 170 180 190 200 210 220 230
 CCGGCTCTGGGGGCTCTCCCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCACCGAGG
 240 250 X

1520 1530 1540 1550 1560 1570 1580
 TTCTGCCCCAAATACCGAGGACACTGGAGGTGCTAGCAGTGAAGACAGCCTGATGACCACTTCCTGCGCA
 100 110 120 130 140 150 160
 1590 1600 1610 1620 1630 1640 1650
 GGCCTTAAGCTGGAGTCCCTTCCTTAATGACACAGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCA
 170 180 190 200 210 220 230
 GGCCTTAAGCTGGAGTCCCTTCCTTAATGACACAGTGGGTGCTGGAGGAGTGGCTGCTCCACCTCCA
 1660 1670 1680 1690 1700 1710 1720
 CCGGCTCTGGGGGCTCTCCCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCACCGAGG
 170 180 190 200 210 220 230
 CCGGCTCTGGGGGCTCTCCCTGTGATGTCTCCGTACGTGTGGTGGTGAGCCACCGAGG
 240 250 X

38. US-09-030-606-110 (1-3410)
 US-09-071-710-8 Sequence 8, Application US/09071710

Initial Score = 251 Optimized Score = 328 Significance = 0.94
 Residue Identity = 97% Matches = 333 Mismatches = 7
 Gaps = 2 Conservative Substitutions = 0

2160 2170 2180 2190 2200 2210 2220
 CCTGCTGAGGCGCTTCCAGGGGTTTTCAGTCTGAGCTTATACAGGAGGCGCAGAGGGTCCCATGCACTG
 2230 2240 2250 2260 2270 2280 2290 2300
 GAATCGGGGACTCTGCAAGTGGATTACCCAGGCTCAGGGTTAAACAGTAGCTCTAGTTGAGACACCT
 2310 2320 2330 2340 2350 2360 2370
 AGAGAAGGTTTTCAGGAGTGAATAAATCACTAGTCACTGTTTCCCATCTTAAGCCCCCTTAACCTGACG
 2380 2390 2400 2410 2420 2430 2440
 TTCTGTTTATGTAGTCTTGGAGTGGAGTTTCTAGGATGAACACTCTCCATGGGATTGAACATATG
 2450 2460 2470 2480 2490 2500 2510
 CTTATTGTAGGGAAGTCTCTGAGGGCAACACACAGAACAGGTCCTCAGCCCAAGCACTGCTCTT
 2520 2530 2540 2550 2560 2570 2580
 TTTGCTGATCCACCCCTCTTACCTTTTATCAGGATGGCTGTGTGCTCTTCTGTGCTATCAGAGA
 2590
 CACAGGCATT

39. US-09-030-606-110 (1-3410)
 US-09-071-710-4 Sequence 4, Application US/09071710

Initial Score = 247 Optimized Score = 247 Significance = 0.92
 Residue Identity = 100% Matches = 247 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0

1550 1560 1570 1580 1590 1600 1610
GCACTGAGGACAGCCTGATGACCAAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGACACG
|||||
GCTCCCTTCCCTAATGACACG
X 10 20

1620 1630 1640 1650 1660 1670 1680 1690
TGGTGCTGGAGGAGTGGCTGTCTCCACCTCCACCGCGCTGTGGGGCGGCTCTGCTGTGATGCTCCG
|||||
TGGTGCTGGAGGAGTGGCTGTCTCCACCTCCACCGCGCTGTGGGGCGGCTCTGCTGTGATGCTCCG
30 40 50 60 70 80 90

1700 1710 1720 1730 1740 1750 1760
TACGTGTGGTGGTGAGCCCAACCGAGGCGAGGTGGTTCGGGGCGGCGGATCTGCTGGACCTCGCCA
|||||
TACGTGTGGTGGTGAGCCCAACCGAGGCGAGGTGGTTCGGGGCGGCGGATCTGCTGGACCTCGCCA
100 110 120 130 140 150 160

1770 1780 1790 1800 1810 1820 1830
TCCTGGATAGTGCCTTCTGTCTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCACAGCTCAGCC
|||||
TCCTGGATAGTGCCTTCTGTCTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCACAGCTCAGCC
170 180 190 200 210 220 230

1840 X 1850 1860 1870 1880 1890
AGCTGTCACTGCCTATATGATGTCTGCCGAGGCGCTGGGTCTGTGTCGCCATTACTTT
|||||
AGCTGTCA
240 X

40. US-09-030-606-110 (1-3410)

US-09-525-397-4 Sequence 4, Application US/09525397

Initial Score = 247 Optimized Score = 247 Significance = 0.92
Residue Identity = 100% Matches = 247 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

1550 1560 1570 1580 1590 1600 1610
GCACTGAGGACAGCCTGATGACCAAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGACACG
|||||
GCTCCCTTCCCTAATGACACG
X 10 20

1620 1630 1640 1650 1660 1670 1680 1690
TGGTGCTGGAGGAGTGGCTGTCTCCACCTCCACCGCGCTGTGGGGCGGCTCTGCTGTGATGCTCCG
|||||
TGGTGCTGGAGGAGTGGCTGTCTCCACCTCCACCGCGCTGTGGGGCGGCTCTGCTGTGATGCTCCG
30 40 50 60 70 80 90

1700 1710 1720 1730 1740 1750 1760
TACGTGTGGTGGTGAGCCCAACCGAGGCGAGGTGGTTCGGGGCGGCGGATCTGCTGGACCTCGCCA
|||||
TACGTGTGGTGGTGAGCCCAACCGAGGCGAGGTGGTTCGGGGCGGCGGATCTGCTGGACCTCGCCA
100 110 120 130 140 150 160

1770 1780 1790 1800 1810 1820 1830
TCCTGGATAGTGCCTTCTGTCTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCACAGCTCAGCC
|||||
TCCTGGATAGTGCCTTCTGTCTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCACAGCTCAGCC
170 180 190 200 210 220 230

1840 X 1850 1860 1870 1880 1890
AGCTGTCACTGCCTATATGATGTCTGCCGAGGCGCTGGGTCTGTGTCGCCATTACTTT
|||||
AGCTGTCA
240 X

41. US-09-030-606-110 (1-3410)

US-08-850-713-5 Sequence 5, Application US/08850713

Initial Score = 247 Optimized Score = 247 Significance = 0.92

Residue Identity = 100% Matches = 247 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

1550 1560 1570 1580 1590 1600 1610
GCACTGAGGACAGCCTGATGACCAAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGACACG
|||||
GCTCCCTTCCCTAATGACACG
X 10 20

1620 1630 1640 1650 1660 1670 1680 1690
TGGTGCTGGAGGAGTGGCTGTCTCCACCTCCACCGCGCTGTGGGGCGGCTCTGCTGTGATGCTCCG
|||||
TGGTGCTGGAGGAGTGGCTGTCTCCACCTCCACCGCGCTGTGGGGCGGCTCTGCTGTGATGCTCCG
30 40 50 60 70 80 90

1700 1710 1720 1730 1740 1750 1760
TACGTGTGGTGGTGAGCCCAACCGAGGCGAGGTGGTTCGGGGCGGCGGATCTGCTGGACCTCGCCA
|||||
TACGTGTGGTGGTGAGCCCAACCGAGGCGAGGTGGTTCGGGGCGGCGGATCTGCTGGACCTCGCCA
100 110 120 130 140 150 160

1770 1780 1790 1800 1810 1820 1830
TCCTGGATAGTGCCTTCTGTCTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCACAGCTCAGCC
|||||
TCCTGGATAGTGCCTTCTGTCTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCACAGCTCAGCC
170 180 190 200 210 220 230

1840 X 1850 1860 1870 1880 1890
AGCTGTCACTGCCTATATGATGTCTGCCGAGGCGCTGGGTCTGTGTCGCCATTACTTT
|||||
AGCTGTCA
240 X

42. US-09-030-606-110 (1-3410)

US-09-841-894A-4 Sequence 4, Application US/09841894A

Initial Score = 247 Optimized Score = 247 Significance = 0.92
Residue Identity = 100% Matches = 247 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

1550 1560 1570 1580 1590 1600 1610
GCACTGAGGACAGCCTGATGACCAAGCTTCCTGCCAGGCCCTAAGCCTGGAGCTCCCTTCCCTAATGACACG
|||||
GCTCCCTTCCCTAATGACACG
X 10 20

1620 1630 1640 1650 1660 1670 1680 1690
TGGTGCTGGAGGAGTGGCTGTCTCCACCTCCACCGCGCTGTGGGGCGGCTCTGCTGTGATGCTCCG
|||||
TGGTGCTGGAGGAGTGGCTGTCTCCACCTCCACCGCGCTGTGGGGCGGCTCTGCTGTGATGCTCCG
30 40 50 60 70 80 90

1700 1710 1720 1730 1740 1750 1760
TACGTGTGGTGGTGAGCCCAACCGAGGCGAGGTGGTTCGGGGCGGCGGATCTGCTGGACCTCGCCA
|||||
TACGTGTGGTGGTGAGCCCAACCGAGGCGAGGTGGTTCGGGGCGGCGGATCTGCTGGACCTCGCCA
100 110 120 130 140 150 160

1770 1780 1790 1800 1810 1820 1830
TCCTGGATAGTGCCTTCTGTCTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCACAGCTCAGCC
|||||
TCCTGGATAGTGCCTTCTGTCTCCAGGTGGCCCATCCCTGTTTATGGGCTCCATTGTCACAGCTCAGCC
170 180 190 200 210 220 230

1840 X 1850 1860 1870 1880 1890
AGCTGTCACTGCCTATATGATGTCTGCCGAGGCGCTGGGTCTGTGTCGCCATTACTTT
|||||
AGCTGTCA
240 X

43. US-09-030-606-110 (1-3410)

US-08-850-713-9 Sequence 9, Application US/08850713

Initial Score = 218 Optimized Score = 242 Significance = 0.76
Residue Identity = 98% Matches = 247 Mismatches = 1
Gaps = 2 Conservative Substitutions = 0

2190 2200 2210 2220 2230 2240 2250 2260
TGGACATTATACAGGAGCCAGAGGGCTCCATGCATGGAATGCGGAGCTCTCAGGTGATTACCCAGG
|||||
CTCTGCAGGTGATTACCCAGG
X
20

2270 2280 2290 2300 2310 2320 2330
CTCAGGTTAAACAGCTAGCTCTAGTTGAGACACACCTAGAGAGGGTTTTGGGAGCTGAATAAATCTCAG
|||||
CTCAGGTTAAACAGCTAGCTCTAGTTGAGACACACCTAGAGAGGGTTTTGGGAGCTGAATAAATCTCAG
30 40 50 60 70 80 90

2340 2350 2360 2370 2380 2390 2400
TCACCTGGTTTCCCATCTCTAAGCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTCATGGGAGTTCT
|||||
TCACCTGGTTTCCCATCTCTAAGCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTCATGGGAGTTCT
100 110 120 130 140 150 160

2410 2420 2430 2440 2450 2460 2470
AGGATGAACACCTCCATGGGATTGAACATATG--ACTTATTTGTAGGGAAGAGTCTCGAGGGGCAAC.
|||||
AGGATGAACACCTCCATGGGATTGAACATATGAAAGTTATTTGTAGGGAAGAGTCTCGAGGGGCAAC
170 180 190 200 210 220 230

2480 X 2500 2510 2520 2530
ACACAAGAACAGAGTCCCTCAGCCCCACAGCACTGCTCTTTTCTGATCCACCCCTCTTA
|||||
ACACAAGAACCA
240 250

44. US-09-030-606-110 (1-3410)

US-09-071-710-2 Sequence 2, Application US/09071710

Initial Score = 217 Optimized Score = 217 Significance = 0.76
Residue Identity = 100% Matches = 217 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

1140 1150 1160 1170 1180 1190 1200
ACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGGCGAGGGGCTGTACACGGCGCTGCCAGAGCTGA
|||||
ACACGGCGCTGCCAGAGCTGA
X
20

1210 1220 1230 1240 1250 1260 1270
GCCGGCACCGAGCCGGAGACACTATGATGAGCGTTTCGGATGGGAGCCTGGGGCTGTTCTTCGACGTG
|||||
GCCGGCACCGAGCCGGAGACACTATGATGAGCGTTTCGGATGGGAGCCTGGGGCTGTTCTTCGACGTG
30 40 50 60 70 80 90

1280 1290 1300 1310 1320 1330 1340 1350
CGCCATCTCCCTGCTCTCTCTGTCATGACCGGCTGTGTCAGCGATTCGCACTCGAGCAGTCTATTT
|||||
CGCCATCTCCCTGCTCTCTCTGTCATGACCGGCTGTGTCAGCGATTCGCACTCGAGCAGTCTATTT
100 110 120 130 140 150 160

1360 1370 1380 1390 1400 1410 1420
GGCCAGTGTGGCAGCTTCCCTGCTGGGTGCGGTGCCACATGCTTCCACACAGTGTGGCGGTGGTGACAGC
|||||
GGCCAGTGTGGCAGCTTCCCTGCTGGGTGCGGTGCCACATGCTTCCACACAGTGTGGCGGTGGTGACAGC
170 180 190 200 210 220 X

1430 1440 1450
TTCAGCCGCCCTCACCAGGTTTACCTTCT

45. US-09-030-606-110 (1-3410)

US-09-525-397-2 Sequence 2, Application US/09525397

Initial Score = 217 Optimized Score = 217 Significance = 0.76
Residue Identity = 100% Matches = 217 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

1140 1150 1160 1170 1180 1190 1200
ACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGGCGAGGGGCTGTACACGGCGCTGCCAGAGCTGA
|||||
ACCAGGGCGTCCCCAGAGCTGA
X
20

1210 1220 1230 1240 1250 1260 1270
GCCGGCACCGAGCCGGAGACACTATGATGAAGCGCTTCGATGGGAGCCTGGGGCTGTTCTTCGAGTG
|||||
GCCGGCACCGAGCCGGAGACACTATGATGAAGCGCTTCGATGGGAGCCTGGGGCTGTTCTTCGAGTG
30 40 50 60 70 80 90

1280 1290 1300 1310 1320 1330 1340 1350
CGCCATCTCCCTGCTCTCTCTGTCATGACCGGCTGTGTCAGCGATTCGCACTCGAGCAGTCTATTT
|||||
CGCCATCTCCCTGCTCTCTCTGTCATGACCGGCTGTGTCAGCGATTCGCACTCGAGCAGTCTATTT
100 110 120 130 140 150 160

1360 1370 1380 1390 1400 1410 1420
GGCCAGTGTGGCAGCTTCCCTGCTGGGTGCCAGCTGCTGCCACAGTGTGGCGGTGGTGACAGC
|||||
GGCCAGTGTGGCAGCTTCCCTGCTGGGTGCCAGCTGCTGCCAGCTGCTGCCAGCTGCTGCCAGC
170 180 190 200 210 X

1430 1440 1450
TTCAGCCGCCCTCACCAGGTTTACCTTCT

46. US-09-030-606-110 (1-3410)

US-08-850-713-2 Sequence 2, Application US/08850713

Initial Score = 217 Optimized Score = 217 Significance = 0.76
Residue Identity = 100% Matches = 217 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

1140 1150 1160 1170 1180 1190 1200
ACTCATGACCTTCACGCTGTTTACACGGATTTCGTGGGCGAGGGGCTGTACACGGCGCTGCCAGAGCTGA
|||||
ACCAGGGCGTCCCCAGAGCTGA
X
20

1210 1220 1230 1240 1250 1260 1270
GCCGGCACCGAGCCGGAGACACTATGATGAAGCGTTTCGGATGGGAGCCTGGGGCTGTTCTTCGACGTG
|||||
GCCGGCACCGAGCCGGAGACACTATGATGAAGCGTTTCGGATGGGAGCCTGGGGCTGTTCTTCGACGTG
30 40 50 60 70 80 90

1280 1290 1300 1310 1320 1330 1340 1350
CGCCATCTCCCTGCTCTCTCTGTCATGACCGGCTGTGTCAGCGATTCGCACTCGAGCAGTCTATTT
|||||
CGCCATCTCCCTGCTCTCTCTGTCATGACCGGCTGTGTCAGCGATTCGCACTCGAGCAGTCTATTT
100 110 120 130 140 150 160

1360 1370 1380 1390 1400 1410 1420
GGCCAGTGTGGCAGCTTCCCTGCTGGGTGCCAGCTGCTGCCACAGTGTGGCGGTGGTGACAGC
|||||
GGCCAGTGTGGCAGCTTCCCTGCTGGGTGCCAGCTGCTGCCACAGTGTGGCGGTGGTGACAGC
170 180 190 200 210 X

1430 1440 1450
TTCAGCCGCCCTCACCAGGTTTACCTTCT

47. US-09-030-606-110 (1-3410)

US-09-841-894A-2 Sequence 2, Application US/09841894A

Initial Score = 217 Optimized Score = 217 Significance = 0.76


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3140 3150 3160 3170 3180 3190 3200
GAAATCTCACAGAAACTCAGGAGCACCCTGCTGAGTAAAGGAGGCTTATCTCTCAGGGGGGTTT
|||||
3140 3150 3160 3170 3180 3190 3200
GAAATCTCACAGAAACTCAGGAGCACCCTGCTGAGTAAAGGAGGCTTATCTCTCAGGGGGGTTT
30 40 50 60 70 80 90
GAAATCTCACAGAAACTCAGGAGCACCCTGCTGAGTAAAGGAGGCTTATCTCTCAGGGGGGTTT
|||||
3210 3220 3230 3240 3250 3260 3270
AAGTGCCTGTTTCAATAATGCTGCTTATTTATTTAGCGGGTGAATATTTTAACTAGTGAAGAATCA
|||||
3210 3220 3230 3240 3250 3260 3270
AAGTGCCTGTTTCAATAATGCTGCTTATTTATTTAGCGGGTGAATATTTTAACTAGTGAAGAATCA
100 110 120 130 140 150 160
AAGTGCCTGTTTCAATAATGCTGCTTATTTATTTAGCGGGTGAATATTTTAACTAGTGAAGAATCA
|||||
3280 3290 3300 3310 3320 3330 3340 3350
GAGTATAATGTTTATGGTGACAAAATTAAGGCTTCTTATATGTTTAAAAA
|||||
3280 3290 3300 3310 3320 3330 3340 3350
GAGTATAATGTTTATGGTGACAAAATTAAGGCTTCTTATATGTTT
170 180 190 200 210 X
GAGTATAATGTTTATGGTGACAAAATTAAGGCTTCTTATATGTTT
|||||
3360 3370
AAAAAAAAAAAAAAAAAAAAA

```

52. US-09-030-606-110 (1-3410)
US-09-841-894A-1 Sequence 14, Application US/09841894A

```

Initial Score = 213 Optimized Score = 213 Significance = 0.74
Residue Identity = 100% Matches = 213 Mismatches = 0
Gaps = 0 Conservative Substitutions = 0

3070 3080 3090 3100 3110 3120 3130
AGGACGAGACGACAAAGTGGCGGTTTCCCAAGCCCTTGTCATCAGGCCCCAGAGTATATCTGTGTGG
|||||
3070 3080 3090 3100 3110 3120 3130
AGGACGAGACGACAAAGTGGCGGTTTCCCAAGCCCTTGTCATCAGGCCCCAGAGTATATCTGTGTGG
|||||
3140 3150 3160 3170 3180 3190 3200
GGAATCTCACAGAAACTCAGGAGCACCCTGCTGAGTAAAGGAGGCTTATCTCTCAGGGGGGTTT
|||||
3140 3150 3160 3170 3180 3190 3200
GGAATCTCACAGAAACTCAGGAGCACCCTGCTGAGTAAAGGAGGCTTATCTCTCAGGGGGGTTT
30 40 50 60 70 80 90
GGAATCTCACAGAAACTCAGGAGCACCCTGCTGAGTAAAGGAGGCTTATCTCTCAGGGGGGTTT
|||||
3210 3220 3230 3240 3250 3260 3270
AAGTGCCTGTTTCAATAATGCTGCTTATTTATTTAGCGGGTGAATATTTTAACTAGTGAAGAATCA
|||||
3210 3220 3230 3240 3250 3260 3270
AAGTGCCTGTTTCAATAATGCTGCTTATTTATTTAGCGGGTGAATATTTTAACTAGTGAAGAATCA
100 110 120 130 140 150 160
AAGTGCCTGTTTCAATAATGCTGCTTATTTATTTAGCGGGTGAATATTTTAACTAGTGAAGAATCA
|||||
3280 3290 3300 3310 3320 3330 3340 3350
GAGTATAATGTTTATGGTGACAAAATTAAGGCTTCTTATATGTTTAAAAA
|||||
3280 3290 3300 3310 3320 3330 3340 3350
GAGTATAATGTTTATGGTGACAAAATTAAGGCTTCTTATATGTTT
170 180 190 200 210 X
GAGTATAATGTTTATGGTGACAAAATTAAGGCTTCTTATATGTTT
|||||
3360 3370
AAAAAAAAAAAAAAAAAAAAA

```

53. US-09-030-606-110 (1-3410)
US-08-850-713-6 Sequence 6, Application US/08850713

```

Initial Score = 206 Optimized Score = 211 Significance = 0.70
Residue Identity = 96% Matches = 211 Mismatches = 7
Gaps = 0 Conservative Substitutions = 0

1610 1620 1630 1640 1650 1660 1670
CCCTAATGGACACGCTGGTGTGGAGGAGTGGCTGTCTCCACCTCCAGCGGCTCTCGGGGGCTCTGC
|||||
1610 1620 1630 1640 1650 1660 1670
CCCTAATGGACACGCTGGTGTGGAGGAGTGGCTGTCTCCACCTCCAGCGGCTCTCGGGGGCTCTGC
100 110 120 130 140 150 160
CCCTAATGGACACGCTGGTGTGGAGGAGTGGCTGTCTCCACCTCCAGCGGCTCTCGGGGGCTCTGC
X

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```

1680 1690 1700 1710 1720 1730 1740
CTGTGATGTCCTCGTACGTGTGGTGTAGCCACCGAGGCGAGGTGTTCCTCGGGCCGGGCGCATCTG
|||||
1680 1690 1700 1710 1720 1730 1740
CTGTGATGTCCTCGTACGTGTGGTGTAGCCACCGAGGCGAGGTGTTCCTCGGGCCGGGCGCATCTG
30 40 50 60 70 80 90
CTGTGATGTCCTCGTACGTGTGGTGTAGCCACCGAGGCGAGGTGTTCCTCGGGCCGGGCGCATCTG
|||||
1750 1760 1770 1780 1790 1800 1810 1820
CCTGGACCTGCCCATCTGATAGTGCCTTCTCTGCTGCCAGTGGCCCCCATCCCTGTTTATGGGCTCCAT
|||||
1750 1760 1770 1780 1790 1800 1810 1820
CCTGGACCTGCCCATCTGATAGTGCCTTCTCTGCTGCCAGTGGCCCCCATCCCTGTTTATGGGCTCCAT
100 110 120 130 140 150 160
CCTGGACCTGCCCATCTGATAGTGCCTTCTCTGCTGCCAGTGGCCCCCATCCCTGTTTATGGGCTCCAT
|||||
1830 1840 1850 1860 1870 X 1880 1890
TGTCACGCTCAGCAGTCTGCTACTGCCTATATGGTGTGCCGAGGCTGTGGTCTGCGCATTTACTT
|||||
1830 1840 1850 1860 1870 X 1880 1890
TGTCACGCTCAGCAGTCTGCTACTGCCTATATGGTGTGCCGAGGCTGTGGTCTGCGCATTTACTT
170 180 190 200 210 X
TGTCACGCTCAGCAGTCTGCTACTGCCTATATGGTGTGCCGAGGCTGTGGTCTGCGCATTTACTT
|||||
1900 1910 1920
TGCTACACAGGTAGTATTTGACAGAGCGGA

```

54. US-09-030-606-110 (1-3410)
US-08-850-713-12 Sequence 12, Application US/08850713

```

Initial Score = 203 Optimized Score = 203 Significance = 0.68
Residue Identity = 98% Matches = 203 Mismatches = 4
Gaps = 0 Conservative Substitutions = 0

2790 2800 2810 2820 2830 2840 2850
GACCTTGGAATTTACTCATCCCAATGATTAATCCAAATGCTTTACCAAGTTAGGTGTGTAAGGAA
|||||
2790 2800 2810 2820 2830 2840 2850
GACCTTGGAATTTACTCATCCCAATGATTAATCCAAATGCTTTACCAAGTTAGGTGTGTAAGGAA
|||||
2860 2870 2880 2890 2900 2910 2920 2930
GGTAGAGGTGGGCTTCAAGCTCTCAAGGCTTCCCTAACCCACCCCTCTCTCTTGTGGCCAGCTGGTCCC
|||||
2860 2870 2880 2890 2900 2910 2920 2930
GGTAGAGGTGGGCTTCAAGCTCTCAAGGCTTCCCTAACCCACCCCTCTCTCTTGTGGCCAGCTGGTCCC
30 40 50 60 70 80 90
GGTAGAGGTGGGCTTCAAGCTCTCAAGGCTTCCCTAACCCACCCCTCTCTCTTGTGGCCAGCTGGTCCC
|||||
2940 2950 2960 2970 2980 2990 3000
CCCACCTTCCCTCCCTCTACTCTCTAGGACTGGGCTGATGAAGCAGCTGCCAAATTTCCCTACCC
|||||
2940 2950 2960 2970 2980 2990 3000
CCCACCTTCCCTCCCTCTACTCTCTAGGACTGGGCTGATGAAGCAGCTGCCAAATTTCCCTACCC
|||||
3010 3020 3030 3040 X 3050 3060 3070
CAACTTTCCTCCCTTACCCCAACTTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGC
|||||
3010 3020 3030 3040 X 3050 3060 3070
CAACTTTCCTCCCTTACCCCAACTTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGC
170 180 190 200 X
CAACTTTCCTCCCTTACCCCAACTTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGCTTCCCAAGC
3080 3090
ACAAAGTGGGTTTCCCAA

```

55. US-09-030-606-110 (1-3410)
US-08-850-713-7 Sequence 7, Application US/08850713

```

Initial Score = 187 Optimized Score = 219 Significance = 0.60
Residue Identity = 99% Matches = 224 Mismatches = 0
Gaps = 1 Conservative Substitutions = 0

1790 1800 1810 1820 1830 X 1840 1850
GCTGTCCAGTGGCCCCATCCCTGTTTATGGGCTCCATTTCCAGCTCAGCTGCTGCTACTGCTCTATAT
|||||
1790 1800 1810 1820 1830 X 1840 1850
GCTGTCCAGTGGCCCCATCCCTGTTTATGGGCTCCATTTCCAGCTCAGCTGCTGCTACTGCTCTATAT
100 110 120 130 140 150 160
GCTGTCCAGTGGCCCCATCCCTGTTTATGGGCTCCATTTCCAGCTCAGCTGCTGCTACTGCTCTATAT
X
1860 1870 1880 1890 1900 1910 1920
GCTGTCCAGGCGCTGGTCTGTGTCCTCCATTTACTTTGTACAGGTAGTATTTACAGAGGAGGCTT
|||||
1860 1870 1880 1890 1900 1910 1920
GCTGTCCAGGCGCTGGTCTGTGTCCTCCATTTACTTTGTACAGGTAGTATTTACAGAGGAGGCTT
|||||

```


2130 2140 2150 2160 2170 2180 2190 2200
TCTCCTCTCTCCCCAGCTCTTAGGGTGCCTGACTGGAGGCCCTCCAAAGGGGTTTCAGCTCTGGACTTTATAC
TCTCCTCTCTCCCCAGCTCTTAGGGTGCCTGACTGGAGGCCCTCCAAAGGGGTTTCAGCTCTGGACTTTATAC
100 110 120 130 140 150 160

[illegible]

3210 3220 3230
CGTTTACCTCCCTTTGCAATAATGTCGCTTATT

3350 3360 3370 3380 3390 3400 3410
AA

GGAATTCCTCCAAATCTCTTCGNTCTTGGGCTTCTNCTGATGCCCTTANCTGGTTGCCGNGNATGCCAANCAACC
 460 470 480 490 500 510 520
 1380 1390 1400 1410 1420 1430 1440
 CTGTGGCTGCGGTGCCACATGCTGTCCACAGTGTGGCGTGTGACAGCTTTCAGCGCCCTTCACCGGT
 1450 1460 1470 1480 1490 1500 1510
 CCAANCCCGGGGTCCCAANCAACCCNCCTCTCTTTCATCTG-----GGTTTNTTCCCGGACGNTGG
 530 540 550 560 570 580 590
 1450 1460 1470 1480 1490 1500 1510
 TCACCTTCTCAGCCCTCAGATCCTGCCCTACAC---ACTGGCCTCCCTCTACACCGGGAGAGAGCTGT
 1520 1530 1540 1550 1560 1570 1580
 TTCCTCTCAAGGGANCCATATCTCNACCAANTACTCACCTNTNCCCCCTGNNACCCANCTCTTANNNGT
 590 600 610 620 630 640 650 660
 1520 1530 1540 1550 1560 1570 1580
 TCCTGCCCAATACCGAGGACACTGAGGTGTAGCAGTGAGGACGCTGATGACGACTTCTTCCGACG
 1590 1600 1610 1620 1630 1640 1650
 TCCNCCCGNCTCTGGCCGNTCAANANGCTTNCANACCTGGGTCTGCC---TTCGCCCTTCCCTATCT
 670 680 690 700 710 720 730
 1590 1600 1610 1620 1630 1640 1650
 GCCCTAAGCCCTGGAGCTCCCTTCCCTAATGACACGCTGGGTGCTGAGGACGCTGCTCCCACTCCAC
 1660 1670 1680 1690 1700 1710 1720
 GNACCCNCNCTTCTCANNT
 740 750 X

74. US-09-030-606-110 (1-3410)

US-08-806-596-14 Sequence 14, Application US/08806596

Initial Score = 83 Optimized Score = 269 Significance = 0.04
 Residue Identity = 36% Matches = 303 Mismatches = 510
 Gaps = 22 Conservative Substitutions = 0

630 640 650 660 670 680 690 700
 ATCCAGGCCCCCTGGAGCTGGCACTGTCTATCTTGGCGTGGGCTGTGGAGCTGTGCTCCCACTCCAC
 710 720 730 740 750 760 770
 TCACCTCAGTGGGCTGTCTGACCTTTCGCGGACCCGAGCACTGTGCGGAGGCTACTGTCT
 780 790 800 810 820 830 840
 ATGCTTTCATGATCAGTCTTGGGCTGTGCTTCCGCGGACCCGAGCACTGTGCGGAGGCTACTGTCT
 850 860 870 880 890 900 910
 TGGCCCTTACCTGGGCAACGAGGAGTGTCTTGGCTGTGCTTCCGCTGTGCTTCCCTCAGCTGGCTAG
 920 930 940 950 960 970 980
 CAGCCACACTGTCTGGGCTGAGGAGGAGCGCTGGGCGCCACCGAGCAGCAAGGGCTGTG- -GGCCCC
 990 1000 1010 1020 1030 1040 1050
 CTCCTTGTGCCCCACCTGTCTCCATGCCGCGGCTGTGGCTTTCGGAACCTTGGCGCCCTCTTCCCGG
 1060 1070 1080 1090 1100 1110 1120
 GAGCACTGTGATGGCCCTTTCATGNNANGGC- -CTGNGGGAAGTCTCTGACNCCANACTGCTCT
 1130 1140 1150 1160 1170 1180 1190
 310 320 330 340 350 360 370 380

1060 1070 1080 1090 1100 1110 1120 1130
 GCTGCACAGCTGTGCTGCCGATCGCCGACCTCGCGGCTCTTGTGGTGTGAGCTGTGAGCTGGAT
 1140 1150 1160 1170 1180 1190 1200
 GGCATCATGACCTTCACGCTGTGTTTACACGGATTGCTGGCGAGGGGTGTACAGGGCTGCCAGAGC
 1210 1220 1230 1240 1250 1260 1270
 TGAGCGGCGACCGGAGGCGCGGAGACACTATGATGAAGCGTTCGGATGGCAGCTGGGCTGTCTCTGCA
 1280 1290 1300 1310 1320 1330 1340
 GTGGCCCATC- -TCCTGTGTCTTCTCTGTGTGATGAGCGGCTGTGAGGATTTCGGCACTCGAGAGTCT
 1350 1360 1370 1380 1390 1400 1410
 ATTTGGCAGTGTGGCAGCTTTCCTGTGTGCTGGCGGTGCCACATGCTGCCACAGTGTGGCGCTGGTGA
 1420 1430 1440 1450 1460 1470 1480 1490
 CAGCTTCAGCGCCCTCAGCGGTTTACCTTCTCAGCCCTGCAGCTGTGCCCTTACACACTGGCTCCCTCT
 1500 1510 1520 1530 1540 1550 1560
 ACCACCGGAGAACAGGAGTGTCTGCCAAATACCGGGGACACTGGAGTGTGCTAGGAGTGTGCTAGGACAGC
 1570 1580 1590 1600 1610 1620 1630
 CCCACGGGTTTCNGTGTGTTNG
 800 810 X

75. US-09-030-606-110 (1-3410)

US-08-904-809-14 Sequence 14, Application US/08904809

Initial Score = 83 Optimized Score = 269 Significance = 0.04
 Residue Identity = 36% Matches = 303 Mismatches = 510
 Gaps = 22 Conservative Substitutions = 0

630 640 650 660 670 680 690 700
 ATCCAGGCCCCCTGGAGCTGGCACTGTCTATCTTCCCTGGGCTGGGCTGTGAGTGTGCTAGGAGTGTGCT
 710 720 730 740 750 760 770
 TCACCTCAGTGGGCTGTCTGACCTTTCGCGGACCCGAGCACTGTGCGGAGGCTACTGTCT
 780 790 800 810 820 830 840
 ATGCTTTCATGATCAGTCTTGGGCTGTGCTTCCCTGTGCTTCCCTGCCATTCAGTGGGACAGGCTGCC
 850 860 870 880 890 900 910
 TGGCCCTTACCTGGGCAACGAGGAGTGTCTTGGCTGTGCTTCCCTCAGCTTCTTCCCTCAGCTGGTAG
 920 930 940 950 960 970 980
 CAGCCACACTGTCTGGGCTGAGGAGGAGCGCTGGGCGCCACCGAGCAGCAAGGGCTGTG- -GGCCCC
 990 1000 1010 1020 1030 1040 1050
 CTCCTTGTGCCCCACCTGTCTCCATGCCGCGGCTGTGGCTTTCGGAACCTTGGCGCCCTCTTCCCGG
 1060 1070 1080 1090 1100 1110 1120
 GAGCACTGTGATGGCCCTTTCATGNNANGGC- -CTGNGGGAAGTCTCTGACNCCANACTGCTCT
 1130 1140 1150 1160 1170 1180 1190
 310 320 330 340 350 360 370 380

170	180	190	200	210	220	230
920	930	940	950	960	970	980
CAGCCACACTGCTGGTGTAGGAGGACGCGCTGGGCCACCGAGCAGAGAGGGCTGTC--GGCCCC						
CTTTCACACTCCAGGAACACTGTCNATGCAGACGACCATGCTGCACCGGAAGTGGTGGGCTGACANGTGC	240	250	260	270	280	290
990	1000	1010	1020	1030	1040	1050
CTCTCTGTGCCCCACTGCTGTCGCGCATGCGGGCCGCGTGTGCTTCGCGAACCTGGGCGCGCTTCCTCCCG						
GAGCACACTGGATGGGGCTTTCCATGNNANGGC-CCTGNGGGAAAGTCCCTGANCCTCCANANCTGCCTCT	310	320	330	340	350	360
370	380	390	400	410	420	430
440	450	460	470	480	490	500
510	520	530	540	550	560	570
580	590	600	610	620	630	640
650	660	670	680	690	700	710
720	730	740	750	760	770	780
790	800	810	820	830	840	850
860	870	880	890	900	910	920
930	940	950	960	970	980	990
1000	1010	1020	1030	1040	1050	1060
1070	1080	1090	1100	1110	1120	1130
1140	1150	1160	1170	1180	1190	1200
1210	1220	1230	1240	1250	1260	1270
1280	1290	1300	1310	1320	1330	1340
1350	1360	1370	1380	1390	1400	1410
1420	1430	1440	1450	1460	1470	1480
1490	1500	1510	1520	1530	1540	1550
1560	1570	1580	1590	1600	1610	1620
1630	1640	1650	1660	1670	1680	1690
1700	1710	1720	1730	1740	1750	1760
1770	1780	1790	1800	1810	1820	1830
1840	1850	1860	1870	1880	1890	1900
1910	1920	1930	1940	1950	1960	1970
1980	1990	2000	2010	2020	2030	2040
2050	2060	2070	2080	2090	2100	2110
2120	2130	2140	2150	2160	2170	2180
2190	2200	2210	2220	2230	2240	2250
2260	2270	2280	2290	2300	2310	2320
2330	2340	2350	2360	2370	2380	2390
2400	2410	2420	2430	2440	2450	2460
2470	2480	2490	2500	2510	2520	2530
2540	2550	2560	2570	2580	2590	2600
2610	2620	2630	2640	2650	2660	2670
2680	2690	2700	2710	2720	2730	2740
2750	2760	2770	2780	2790	2800	2810
2820	2830	2840	2850	2860	2870	2880
2890	2900	2910	2920	2930	2940	2950
2960	2970	2980	2990	3000	3010	3020
3030	3040	3050	3060	3070	3080	3090
3100	3110	3120	3130	3140	3150	3160
3170	3180	3190	3200	3210	3220	3230
3240	3250	3260	3270	3280	3290	3300
3310	3320	3330	3340	3350	3360	3370
3380	3390	3400	3410	3420	3430	3440
3450	3460	3470	3480	3490	3500	3510
3520	3530	3540	3550	3560	3570	3580
3590	3600	3610	3620	3630	3640	3650
3660	3670	3680	3690	3700	3710	3720
3730	3740	3750	3760	3770	3780	3790
3800	3810	3820	3830	3840	3850	3860
3870	3880	3890	3900	3910	3920	3930
3940	3950	3960	3970	3980	3990	4000

```

76. US-09-030-606-110 (1-3410)
US-09-020-747-14 Sequence 14, Application US/09020747

Initial Score = 83 Optimized Score = 269 Significance = 0.04
Residue Identity = 36% Matches = 303 Mismatches = 510
Gaps = 22 Conservative Substitutions = 0

630      640      650      660      670      680      690      700
ATCCAGGCCCTGGAGCTGCACTGCTATCTGGCGTGGGGCTGCTGGACTTCTGGGCCAGGTGTC
|||||
TGCTCTTCTCTCAAAGTTGTTCT
X      10      20

710      720      730      740      750      760      770
TCACACTGGAGGCCCTGCTCTGACCTTTCGGGACCCGGACCACTGTGCGCCAGGCCTACTCTGTC
|||||

```


Thu May 1 15:12:20 2003

```
1380 1390 1400 1410 1420 1430 1440
CTGTGGCTGCCGGTCCACATGCCCTGTCCACAGTGTGGCGGTGGTGACAGCTTACGCCGCCCTCACCGGGT
| | | | | | | | | | | | | | | |
NGNCNGTCANCCNAGGGAAGGGGNNCCNNTGTTGACGTTGNGGNGANGTCCGAANANTCCTCNCNCT
670 680 690 700 710 720 730
1450 1460 1470 1480 1490 1500 1510
TCACCTTCTCAGCCCTGCGAGATCCTGCCCCACACATGCGCTCCCTCTACACCGGGGAGAGAGGTGTCC
| | | | | | | | | | | | | | | |
CANCNTACCCCTCGGGCGNNCTCTCNGTTNCCAACTTANCAANTCTCCCGGNGGNCNCTCTCAGCCTCN
740 750 760 770 780 790 800
1520 1530 1540 1550 1560 1570 1580
TGCCCCAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAGGACAGCCTGATGACCCAGCTTCTGCCAGGCC
| | | | | | | | | | | | | | | |
CCNCCCNCTCTCTGCANTGTNCTCTGCTCTNACCNNTTACGANTTTCCGNCNCCCTCTTTCC
810 820 830 840 850 860 870 X
1590 1600 1610 1620
CTAAGCCTGGAGCTCCCTTCCCTTATGGACACGTGGTGCT
```


> O <
> I O < Intelligenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-030-606-110-inv.res made by tport on Thu 1 May 103 14:53:55-PDT.

Query sequence being compared: US-09-030-606-110' (1-3410)
Number of sequences searched: 410
Number of scores above cutoff: 410

Results of the initial comparison of US-09-030-606-110' (1-3410) with:

File : 6130043.seq
File : 6252047.seq
File : US08806596.seq
File : US08850713.seq
File : US08904809.seq
File : US09020747.seq
File : US09841894A.seq

100-

N - ***

U 50- *

M - *

B - **

E -

R -

O -

F 10- *

S - *

E 5- *

Q - *

U - *

E -

N -

C -

E -

S 0- **

SCORE 0 | 43 | 86 | 129 | 172 | 216 | 259 | 302 | 345 | 388

STDEV -1 0 1 2 3 4 5 6 7 8 9

PARAMETERS

Similarity matrix Unitary K-tuple
Mismatch penalty 1 Joining penalty 4
Gap penalty 5.00 Window size 30
Gap size penalty 0.33
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 39 Median 39 Standard Deviation 24.57
Times: CPU 00:00:02.02 Total Elapsed 00:00:02.00

Number of residues: 189792
Number of sequences searched: 410
Number of scores above cutoff: 410

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.	Frame
1. US-08-806-596-11	Sequence 11, Application	772	388	664	14.21
2. US-08-904-809-11	Sequence 11, Application	772	374	664	13.64
3. US-09-020-747-11	Sequence 11, Application	772	374	564	13.64
4. US-08-904-809-15	Sequence 15, Application	783	160	254	2.48
5. US-09-020-747-10	Sequence 10, Application	470	93	191	2.20
6. US-09-020-747-10	Sequence 106, Application	473	90	180	2.08
7. US-08-904-809-53	Sequence 53, Application	484	87	167	1.95
8. US-09-020-747-53	Sequence 53, Application	484	87	167	1.95
9. US-09-020-747-19	Sequence 19, Application	731	84	231	1.83
10. US-08-806-596-19	Sequence 19, Application	731	83	231	1.79
11. US-09-020-747-10	Sequence 104, Application	578	81	214	1.71
12. US-08-806-596-40	Sequence 40, Application	753	80	233	1.67
13. US-08-904-809-43	Sequence 43, Application	305	77	102	1.55
14. US-09-020-747-43	Sequence 43, Application	305	77	102	1.55
15. US-08-806-596-37	Sequence 37, Application	760	77	157	1.55
16. US-08-904-809-37	Sequence 37, Application	760	77	157	1.55
17. US-09-020-747-37	Sequence 37, Application	760	77	157	1.55
18. US-08-904-809-32	Sequence 32, Application	789	74	264	1.42
19. US-09-020-747-32	Sequence 32, Application	789	74	264	1.42
20. US-09-071-710-15	Sequence 15, Application	2143	73	680	1.38
21. US-09-525-397-15	Sequence 15, Application	2143	73	680	1.38
22. US-09-841-894A-1	Sequence 15, Application	2143	73	680	1.38
23. US-08-904-809-34	Sequence 34, Application	756	72	253	1.34
24. US-09-020-747-17	Sequence 171, Application	1248	71	419	1.30
25. US-09-020-747-17	Sequence 173, Application	1265	71	426	1.30
26. US-09-020-747-17	Sequence 175, Application	1167	70	392	1.26
27. US-08-904-809-72	Sequence 72, Application	511	68	102	1.22
28. US-08-850-713-3	Sequence 3, Application	268	68	102	1.18
29. US-08-806-596-32	Sequence 32, Application	789	67	264	1.14
30. US-09-020-747-10	Sequence 105, Application	538	66	198	1.10
31. US-08-806-596-39	Sequence 39, Application	751	66	228	1.10
32. US-08-904-809-39	Sequence 39, Application	751	66	228	1.10
33. US-09-020-747-39	Sequence 39, Application	751	66	228	1.10
34. US-09-020-747-15	Sequence 15, Application	783	66	251	1.10
35. US-09-020-747-10	Sequence 109, Application	1524	65	461	1.06
36. US-09-020-747-33	Sequence 33, Application	793	63	253	0.98
37. US-08-806-596-2	Sequence 2, Application	816	62	266	0.94
38. US-09-020-747-2	Sequence 2, Application	816	62	266	0.94
39. US-08-806-596-20	Sequence 20, Application	754	61	216	0.90
40. US-08-806-596-27	Sequence 27, Application	818	61	238	0.90
41. US-08-904-809-27	Sequence 27, Application	818	61	238	0.90
42. US-08-904-809-19	Sequence 19, Application	731	60	231	0.85
43. US-08-806-596-18	Sequence 18, Application	802	59	259	0.81
44. US-08-904-809-18	Sequence 18, Application	802	59	259	0.81
45. US-09-020-747-18	Sequence 18, Application	802	59	259	0.81
46. US-09-020-747-10	Sequence 107, Application	1621	59	380	0.81
47. US-09-325-397-11	Sequence 11, Application	272	58	93	0.77
48. US-09-020-747-86	Sequence 86, Application	472	59	143	0.77
49. US-09-020-747-92	Sequence 92, Application	477	58	180	0.77
50. US-08-806-596-34	Sequence 34, Application	756	58	253	0.77
51. US-08-904-809-26	Sequence 26, Application	820	58	244	0.77
52. US-09-020-747-13	Sequence 139, Application	382	57	129	0.73
53. US-09-020-747-80	Sequence 80, Application	476	57	152	0.73
54. US-09-020-747-11	Sequence 111, Application	1289	57	327	0.73
55. US-09-020-747-10	Sequence 100, Application	269	56	97	0.69
56. US-08-850-713-11	Sequence 11, Application	272	56	98	0.69
57. US-09-020-747-13	Sequence 133, Application	278	56	95	0.69
58. US-09-071-710-8	Sequence 8, Application	342	56	117	0.69
59. US-09-525-397-8	Sequence 8, Application	342	56	117	0.69

60. US-09-841-894A-8 Sequence 8, Application U 342 56 117 0.69 0
61. US-08-904-809-52 Sequence 52, Application 491 55 72 0.65 0
62. US-09-020-747-52 Sequence 52, Application 491 55 72 0.65 0
63. US-09-020-747-10 Sequence 103, Application 581 55 201 0.65 0
64. US-08-904-809-12 Sequence 12, Application 751 55 243 0.65 0
65. US-09-020-747-12 Sequence 12, Application 751 55 243 0.65 0
66. US-08-806-596-10 Sequence 10, Application 789 55 271 0.65 0
67. US-08-904-809-10 Sequence 10, Application 789 55 271 0.65 0
68. US-09-020-747-10 Sequence 10, Application 789 55 271 0.65 0
69. US-08-904-809-16 Sequence 16, Application 801 55 262 0.65 0
70. US-09-020-747-11 Sequence 110, Application 3410 55 426 0.65 0
71. US-09-020-747-14 Sequence 149, Application 207 54 76 0.61 0
72. US-09-071-710-4 Sequence 4, Application US 247 54 93 0.61 0
73. US-09-525-397-4 Sequence 4, Application US 247 54 93 0.61 0
74. US-08-850-713-5 Sequence 5, Application US 247 54 93 0.61 0
75. US-09-841-894A-4 Sequence 4, Application U 247 54 93 0.61 0
76. US-08-904-809-2 Sequence 2, Application US 816 54 266 0.61 0
77. US-09-071-710-16 Sequence 16, Application 2152 54 704 0.61 0
78. US-09-525-397-16 Sequence 16, Application 2152 54 704 0.61 0
79. US-09-841-894A-1 Sequence 16, Application 2152 54 704 0.61 0
80. US-08-850-713-16 Sequence 16, Application 2154 54 703 0.61 0

1. US-09-030-606-110' (1-3410)
US-08-806-596-11 Sequence 11, Application US/08806596

Initial Score = 388 Optimized Score = 664 Significance = 14.21
Residue Identity = 90% Matches = 701 Mismatches = 58
Gaps = 13 Conservative Substitutions = 0

680 690 700 710 720 730 740
TGATCAGCCCAATGACCACTATCTCAGGGGACCTGATTGTTGGGATCCCCACCCCTACCCAAATATTAGA
|||||
CCACCCCTACCCAAATATTAGA
X 10 20

750 760 770 780 790 800 810 820
CACCACACAGAAAGCTAGCAATGATCCCTCTACCTTTGTTAAATAAATAGTTAAATTTAAATGCC
|||||
CACCACACAGAAAGCTAGCAATGATCCCTCTACCTTTGTTAAATAAATAGTTAAATTTAAATGCC
30 40 50 60 70 80 90

830 840 850 860 870 880 890
TGTGCTCTGTGATGGCAACAGAGCAAGCCACATCTGTATAAAGGTAAAGGGGGGTGGATCAG
|||||
TGTGCTCTGTGATGGCAACAGAGCAAGCCACATCTGTATAAAGGTAAAGGGGGGTGGATCAG
100 110 120 130 140 150 160

900 910 920 930 940 950 960
CAAAAAGACAGTCTGTGGCTGAGGGGACCTGGTCTTGTGTTGCCCTCAGGACCTCTCCCTACAAA
|||||
CAAAAAGACAGTCTGTGGCTGAGGGGACCTGGTCTTGTGTTGCCCTCAGGACCTCTCCCTACAAA
170 180 190 200 210 220 230

970 980 990 1000 1010 1020 1030
TAA--GTCAATATGTTCAATCCCATGGAGAGTGTTCATCTAGAAATCCCATGCAAGAGCTACATTTAA
|||||
TAACTTTTCAATATGTTCAATCCCATGGAGAGTGTTCATCTAGAAATCCCATGCAAGAGCTACATTTAA
240 250 260 270 280 290 300 310

1040 1050 1060 1070 1080 1090 1100
CGAAGCTGAGGTTAAGGGCTTAGAGATGGGAACCAAGGTGACTGAGTTTATTCAGTCCCAAAAACCTTT
|||||
CGAAGCTGAGGTTAAGGGCTTAGAGATGGGAACCAAGGTGACTGAGTTTATTCAGTCCCAAAAACCTTT
320 330 340 350 360 370 380

1110 1120 1130 1140 1150 1160 1170
CTCTAGTGTGTTCACTAGAGAGTGTGTTTACCTGAGCTGGGTGATTCACCTGCAAGAGTCCCGG
|||||
CTCTAGTGTGTTCACTAGAGAGTGTGTTTACCTGAGCTGGGTGATTCACCTGCAAGAGTCCCGG
390 400 410 420 430 440 450

1180 1190 1200 1210 1220 1230 1240 1250

ATTCCAGTGCATGAGGCCCTTCTGSCCTCCCTGTATAAGTCAGACTGAAACCCCTTTGGAAGGCTCCAGT
|||||
ATTCCAGTGCATGGAACCTTCTGSCCTCCCTGTATAAGTCAGACTGAAACCCCTTTGGAAGGCTCCAGT
460 470 480 490 500 510 520
1260 1270 1280 1290 1300 1310 1320
CAGGAGCCCTTAGAGACTGGGAGAGAGAGGAGCGCCCGCCAGCTGTGCAGCTACGACCTCAG
|||||
CAGGAGCCCTTAGAGACTGGGAGAGAGAGGAGCGCGCCCGCCAGCTGTGCAGCTACGACCTCAG
530 540 550 560 570 580 590
1330 1340 1350 1360 1370 1380 1390
CAGCAGAGGTTGGCAGC-AGAGAGCCACATTTTGGCAGCAACAGAACT---GGCGGCGAGCCCGCAG
|||||
CAGCAGAGGTTGGCAGCAGCAAAACCACTTTTACTTTGGCAGCAACAGAACTNGGGGGGCAACCCCGCAC
600 610 620 630 640 650 660 670
1400 1410 1420 1430 1440 1450
CCCCA-TGGGGCTACAGAGGCGGG---AGCTGGGAGCCCA-GTGGAGCGGCTCTCCACGCC--AATGTGC
|||||
CCCNANGGGGTTTACAGGAANCNGGNAACNTGGACCCCAATTNAGCGAGCCGCCCCCNAAATTTGC
680 690 700 710 720 730 740
1460 1470 1480 X 1490 1500 1510 1520
TGGAAAGTTTCTACGCTGAGTATTGGCCAAAGTCCTCTTGTCAAACTACTCTGTAGCAAGTAATATGG
|||||
TGGAAATTTTCTCTCCCTCAAAATTTTTC
750 760 770 X
1530
CGACCAGA

2. US-09-030-606-110' (1-3410)
US-08-904-809-11 Sequence 11, Application US/08904809

Initial Score = 374 Optimized Score = 664 Significance = 13.64
Residue Identity = 90% Matches = 701 Mismatches = 58
Gaps = 13 Conservative Substitutions = 0

680 690 700 710 720 730 740
TGATCAGCCCAATGACCACTATCTCAGGGGACCTGATTGTTGGGATCCCCACCCCTACCCAAATATTAGA
|||||
CCACCCCTACCCAAATATTAGA
X 10 20

750 760 770 780 790 800 810 820
CACCACACAGAAAGCTAGCAATGATCCCTCTACCTTTGTTAAATAAATAGTTAAATTTAAATGCC
|||||
CACCACACAGAAAGCTAGCAATGATCCCTCTACCTTTGTTAAATAAATAGTTAAATTTAAATGCC
30 40 50 60 70 80 90

830 840 850 860 870 880 890
TGTGCTCTGTGATGGCAACAGAGCAAGCCACATCTGTATAAAGGTAAAGGGGGGTGGATCAG
|||||
TGTGCTCTGTGATGGCAACAGAGCAAGCCACATCTGTATAAAGGTAAAGGGGGGTGGATCAG
100 110 120 130 140 150 160

900 910 920 930 940 950 960
CAAAAAGACAGTCTGTGGCTGAGGGGACCTGGTCTTGTGTTGCCCTCAGGACCTCTCCCTACAAA
|||||
CAAAAAGACAGTCTGTGGCTGAGGGGACCTGGTCTTGTGTTGCCCTCAGGACCTCTCCCTACAAA
170 180 190 200 210 220 230

970 980 990 1000 1010 1020 1030
TAA--GTCAATATGTTCAATCCCATGGAGAGTGTTCATCTAGAAATCCCATGCAAGAGCTACATTTAA
|||||
TAACTTTTCAATATGTTCAATCCCATGGAGAGTGTTCATCTAGAAATCCCATGCAAGAGCTACATTTAA
240 250 260 270 280 290 300 310

1040 1050 1060 1070 1080 1090 1100
CGAAGCTGAGGCTTAAGGGCTTAGAGATGGGAACCAAGGTGACTGAGTTTATTCAGTCTCCCAAAAACCTTT
|||||

540 650 660 670 680 690 700 710
TGGGGGGCCAGACCCAGGAGAGAAGATTCTGGCAATGATCAGCCCAATGACCGCATCTCTCAGGGGACCTCT
CAGCGCTCTNNCTTTGGNNGCAAGNTGGNTCCCTCTCGGGCCCCCGGTGGGGCCNNCTCTTAAGCAAAAC

[illegible]

Initial Score	-	71	Optimized Score	-	426	Significance	=	1.30
Residue Identity	-	38%	Matches	-	490	Mismatches	=	756
Gaps	-		Conservative Substitutions	-	43		=	0

[illegible]

	1900	1910	1920	1930	1940	1950	1960
GGCAGGAACACCTGCTTCTCCCGGTGGTAGAGGGAGGCCACTGTTAGGCGCAGAGTCTCGAGGGCTGAGAA							
AGGCAGTTATCTGATTAAAGAACACTAAAGAGGGGACAGGCTAAAAGCCGCGAGGATGTTCTACACTATANCA							
80 90 100 110 120 130 140							
	1970	1980	1990	2000	2010	2020	2030
GGTGAACCCGGGTGAGGGGGCGGTGAAGCTGCACACGGGCCACACTGTGGGACAGCATGTGGCACACCGCGAC							
GGCGCTATTGGGTTGGCTGGAGGAGCTGTGGAACAATCGANAGATTGGTCTGTGGANATTCGCGCTGGCTAT							
150 160 170 180 190 200 210							
	2040	2050	2060	2070	2080	2090	2100
CACAGGGAAGGTGCCACACTGGCCAAATAGACTGCTCGAGTGCAGGATCGCGATCGCTGCACACGGCGTCCATGAC							
TCCTCATTTGTTATACANAGTG-----AGGTTCTCTGTGTGCCCACTGTTTGAACACCGTTCTTCAATA							
220 230 240 250 260 270 280							
	2110	2120	2130	2140	2150	2160	2170
CAGAGAGAAGACACAGGAGATG-GGCGACTCGAAGACAGCCCGCGCTGCCATCCGAAGCGCTTCATCAT							
ATGATAGAATAGTACACATGAGAACTGAAATGGCCCAACCGAAGAAAGGCCCACTAGATTCCTCAGA							
290 300 310 320 330 340 350							
	2180	2190	2200	2210	2220	2230	2240
AGTGTCCGGGGCTCGGTGCCCGGCTCAGCTCTGGGACGCCCTGGTACAGCCCTGCCACAGCAATCGG							
ANAGCCTTCTTAGGGACAATAACCGGATGAAGAAAGATGGGCTCCTTTGTGC-CCCGCTCTGTTATGATTTCTC							
360 370 380 390 400 410 420							
	2260	2270	2280	2290	2300	2310	2320
TGTAACACAGCGTGAAGGTCATGATGCGATCCAGCTGCACAGTCCAGCCAGAGAGCGCGCGAGGTGCG							
TCCATTGCGACGNAAACCGGTTCTTCTAAGCAACNACGGTGATGATGCGCNAAATAACACCCCTCTTGAA							
430 440 450 460 470 480 490							
	2330	X 2340	2350	2360	2370	2380	
GGGGCATGCGGCAGCACAGCTGTTGCGCCGGGGAAGCAGGGCGGCCCATGTTCCGGGAAGCC							
GNACCNCGGAGGA							
500 510							

Initial Score	=	68	Optimized Score	=	102	Significance	=	1.18e-148
Residue Identity	=	43%	Matches	=	117	Mismatches	=	148
Gaps	=		Conservative Substitutions	=	4		=	0

[illegible]

Initial Score	-	69	Optimized Score	-	170	Significance	=	1.22
Residue Identity	-	36%	Matches	-	197	Mismatches	=	313
Gaps	-	28	Conservative Substitutions	-	0		=	0

	1920	1930	1940	1950	1960	1970	1980
TCCCGTGTAGAGGAGCCACTGTGT - AGGCAGGATCTCGAGGCTCAGAAGGTGAACCCGGTGCAGGCG							
GGCAGCTGTGGCAGCTTTCCTGTGTGCGCGGTGCCACATGCCTGTCCACAGTGTGGCCGTGTGCACAGC							
100 110 120 130 140 150 160							
GGTGAAGCTGTTCACCCAGGCACACTGTGGGACAGGCAATGTGCACGGCAGCACACAGGGAAGCTGCCAC							
NTCAGCGCGCCTCACCGGGTTACCTTCTTCAGCCCTTGCA - GATCCTGCCCTACACACTGTGCCCTCCCTTACC							

	590	600	610	620	630	640	650
720		730	740	750	760	770	780
TTGTTGGGATCCCCCAGCCTACCCAAATATTAGACACCAACAGAAAGCTAGCATGGATTCCTT							
660	670	680	690	700	710	720	
TCGCCCNAGACTTCCTCCNCCNANCACAATTTCTTTTNNTCAGGAACGCGNCCNCCNAAATATGNNNN							

32. US-09-030-606-110' (1-3410)

Initial Score	=	66	Optimized Score	=	228	Significance	=	1.10
Residue Identity	=	34%	Matches	=	267	Mismatches	=	478
Gaps	=		Conservative Substitutions	=	35		=	0

[illegible]

80 90 100 110 120 130 140
TTTTTTTAAACATATAAGAAAGCCTTAATTGTGCACCAATAACATATATCTGATTGTCAC
||||| ||||| | | | | |
ATTTGATTTTTTTTAAATGCTGCACAACAATATTTATTTCA-----TTTGTTCTCTTTAT

[illegible]

AGAGATTAACCTCCCTTACTCAGGACGGGTCTCTGAGTTTCGTGTGAGATTCCCCAACGACAGATT
TGCGCCTTTTTCCTTTTTCTTAGGCCGCCTTAGCTTCTAAATTTGGRACATCAAGCAAGCTGAANCG

ATACCTCGGGGCTG--AGATGGACAAGGCTTTGGGAACCGCACCTTGTCTTCGTCCGTGCAGTAGCTC

[illegible]

ATTAACTGTTGTACAAATTCNNTTCACTTTTAATAATTGTCTNAAGCCTTTAATTAANACTGGGGGGGGTG
300 310 320 330 340 350 360 370

GTGCCTTCATCAGCCCGCATCTTAGAGAGAGTAGAGGGGAGTGGAAGTGGGGGGAACCAGCGCTGGGCCCAAGA
400 410 420 430 440 450 460 470 480 490 500

CTTCCCAACCAACCCCTCTGACAAAAGTGCCTGCGCTCAAAATNATGTCCTCCGGCCTTCCTTTGAACACAC
380 390 400 410 420 430 440

ACAGGGGCGGTTCAGGGGCTCCATTTTAAACGCCACTCCCAC
NGCNGAANGTCTCATTTCCCCCNCCAGGTNAAAATGAAGGTTACCAT--TTTTAACGCCACTCCCAC

[illegible]

55. US-09-030-606-110' (1-3410)
US-09-020-747-10 Sequence 109, Application US/09020747

Initial Score	=	65	Optimized Score	=	451	Significance	=	1.06
Residue Identity	=	31%	Matches	=	494	Mismatches	=	1019
Gaps	=	36	Conservative Substitutions	=			=	0

[illegible]

220 AGAGATAAGACCTCCCTAGCTCAGGAGG-----GGTGCTCTAGTTTCTGTGTAGATATCCCCAGAG 280
230 240 250 260 270 280
240 GGGCCACTGTCTCTGCATCGACTTCATGTTTTTCACGCTGGCGTGCTTCACATCTTTCACGGTCAACAAA 250
250 260 270 280 290 300
300 CACAGATACTCTGGGGCTTGAGATGGACAAAGGCTTGGGAACGACCTTTGTGCTCTCTGGTCTGCTG--- 350
310 320 330 340 350
320 CAGCTGGGGCCCAAGATCGTCATCGTGAGCAAGATGATGAAGACGCTGTTCCTCTCTCTCTCTCTCTCGGC 330
330 340 350 360 370 380
340 -AGTAGCTCCAAACAGGTTTGTGAGCTGGTGGGGAAGTTGGGGTAGGGGAAGTTGGGGTAGGGGAGGAAA 420
350 360 370 380 390 400
360 GTGTGCTGTAGCTATGTGGGTGGCCACGAGGGGCTCTCTGAGGCCACCGGACAGT--GACTTCCCAAGTA 400
370 380 390 400 410 420
380 390 400 410 420 430
390 TTTTGGGCAGTGCCTTCATCAGCCAGTCTTAGACAGAGTAGAGGGAGTGGAAAGTGGGGTAGGGGAGGAGGAAA 490
400 410 420 430 440 450
410 TCCGTGGCGCGCTCTCTACCGCTCCCTACCTCGGAGACTTCTCGGCGAGATCTTCGGCGAGATTCCTCCCGCAGGACATGGACGTGG 480
420 430 440 450 460 470
430 440 450 460 470 480
440 450 460 470 480 490
450 460 470 480 490 500
460 470 480 490 500 510
470 480 490 500 510 520
480 490 500 510 520 530
490 500 510 520 530 540
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670 680 690 700 710 720
680 690 700 710 720 730
690 700 710 720 730 740
700 710 720 730 740 750
710 720 730 740 750 760
720 730 740 750 760 770
730 740 750 760 770 780
740 750 760 770 780 790
750 760 770 780 790 800
760 770 780 790 800 810
770 780 790 800 810 820
780 790 800 810 820 830
790 800 810 820 830 840
800 810 820 830 840 850
810 820 830 840 850 860
820 830 840 850 860 870
830 840 850 860 870 880
840 850 860 870 880 890
850 860 870 880 890 900
860 870 880 890 900 910
870 880 890 900 910 920
880 890 900 910 920 930
890 900 910 920 930 940
900 910 920 930 940 950
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920 930 940 950 960 970
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940 950 960 970 980 990
950 960 970 980 990 1000
960 970 980 990 1000 1010
970 980 990 1000 1010 1020
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1130 1140 1150 1160 1170 1180
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1150 1160 1170 1180 1190 1200
1160 1170 1180 1190 1200 1210
1170 1180 1190 1200 1210 1220
1180 1190 1200 1210 1220 1230
1190 1200 1210 1220 1230 1240
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1280 1290 1300 1310 1320 1330
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1340 1350 1360 1370 1380 1390
1350 1360 1370 1380 1390 1400
1360 1370 1380 1390 1400 1410
1370 1380 1390 1400 1410 1420
1380 1390 1400 1410 1420 1430
1390 1400 1410 1420 1430 1440
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1460 1470 1480 1490 1500 1510
1470 1480 1490 1500 1510 1520
1480 1490 1500 1510 1520 1530
1490 1500 1510 1520 1530 1540
1500 1510 1520 1530 1540 1550
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1570 1580 1590 1600 1610 1620
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1630 1640 1650 1660 1670 1680
1640 1650 1660 1670 1680 1690
1650 1660 1670 1680 1690 1700
1660 1670 1

[illegible][illegible]

GTCCNACCTTTAATGGCCGACCGGCTAATCCCTCCCTCCTCCANTTCNNNNACCCGCTTCCNCCT
 450 460 470 480 490 500 510
 GTTGACACGACAGCTGGGCTTCGGGTGGCGAGCAGCGGCTCACCCACAGCCTCTGGACCACTAGTGGG
 3070 3080 3090 3100 3110 3120 3130
 CNTCTCC-----CCTANCCCGCCGCGGAACCTCTCTTTGCCCTACCAAGGCGCCNNACCGCC
 520 530 540 550 560 570
 3140 3150 3160 3170 3180 3190 3200
 CCAGCGGGTAGGGCTCAGGGGCCGTTTCAGACACTCCAGACACTGCTTCGCTCGGCTCTGCTCCAGAGCT
 3210 3220 3230 3240 3250 3260 3270
 GCGGCTCTCTCTCTGCTCCGCCAACTGCCTAGGAATCAGCCAGGCGCCCATTTCTGCCAGCCCTTTGGT
 ---GCNNNGCANNTTCNCGTCCGCTCCNNCTCTTCNNGTTCGNAAGNTCNCNTNNNNNGNCNNNGTNN
 640 650 660 670 680 690 700
 3280 3290 3300 3310 3320 3330 3340
 GCGGCTCCAGCTTCTAGCCCATGCTCAACACCTGCTGCTGTGGGCACCTCAGTGGGACACCTCTCATCA
 3350 3360 3370 3380 3390 3400 3410
 CTCATGCTGCGCAGCGCGCGGTGTACCCGGGACGAGCGGTGCAGGCTGCTTCCC
 GCGCCNNCCCCGNAATTAAGGCGCTCCNNCTCTCGGCCNC
 780 790 800 810 820
 1. US-09-030-606-110' (1-3410)
 US-08-904-809-27 Sequence 27, Application US/08904809
 ntial Score = 61 Optimized Score = 238 Significance = 0.90
 residue Identity = 31% Matches = 273 Mismatches = 543
 gaps = 38 Conservative Substitutions = 0
 2490 2500 2510 2520 2530 2540 2550
 TGCTCTACGCGAGGTGAGGAAGATGAGGTGAGCGGCAAGAGGCACTCTCTGGTGGCCAGGTAGG
 2560 2570 2580 2590 2600 2610 2620 2630
 GGGCCAGGCACTGTGTCCTCCAGTCAATGGCAGCAGAGGTAGCCAGGACAGCCGCCAGACTGATCATGA
 CTCAGGACCTCTGACTGCTCTGGGCAAGAATCTGTGTTCTTCGAGCGCCAGCAGCGGTGATTC
 30 40 50 60 70 80 90
 2640 2650 2660 2670 2680 2690 2700
 AGGCATACAGACAGTAGGCTGGCAGACAGTGTCCGGGTCCCGAAGAGGTACAGAGCAGGCGCTCCAGTG
 AGCCCTGCCCAACTGATTCTGATGACTCGGATGCTGTGACACCCAAAGGCGCAATAGAGTCCC-----A
 100 110 120 130 140 150 160
 2710 2720 2730 2740 2750 2760 2770
 GAGTGAAGACACCTTGCCACACAGATCCAGCAGCCCCCAGCGGCTTCGGATGAGAAGAGGTACAGAGGTGCCA
 GGGTCCAGGAGGGGCGGCTGTGAGCACTTCGGCGGCTTCACCTTGCCAGCCCTCCCATGAGCTCTGGGC
 170 180 190 200 210 220 230
 2780 2790 2800 2810 2820 2830 2840
 TGGATCGGCCACAGCAGCCCTGTCTAGCCAGCGCGGCTTCGGATGAGAAGAGGTACAGAGGTGCCA
 TGGGTCTCCGCTCCAGGGTCTGCTCTCCANGCANGCCANCAAGTGGCGCTGGGCCACACTGGCTCTCTTC
 240 250 260 270 280 290 300
 2850 2860 2870 2880 2890 2900 2910
 AGGACAGTGGCCAGATGAAGGGCGGCGGCGGCATAGGCTCCAGCCAGTGGTCACTGGCTGAGCCTAGGCTAGG

45. US-09-030-606-110' (1-3410)
US-09-020-747-18 Sequence 18, Application US/09020747

Initial Score =	59	Optimized Score =	259	Significance =	0.81
Residue Identity =	34%	Matches =	283	Mismatches =	507
Gaps	=	19	Conservative Substitutions	=	0

ATCCGAACGCCCTTCATCATAGTGTCTCCGGCGCTCGGTGCGCCGCTCAGCTCTGGCGACAGCCCTGGTACAGC
2160 2170 2180 2190 2200 2210 2220 2230
CCCTCGCCACAGAAATCCCGTGTAAACACAGCTGAGGTCATGAGTCCATCCAGCTGCACAGCTCAGCCACG
2240 2250 2260 2270 2280 2290 2300
GNAGCCACGAAGCAGCTCAGCATACAGCCCTCAATCACAGGTCTTCCAGCTGCCGACATTAACGACGGC
2310 2320 2330 2340 2350 2360
AAGAGCCGCGCAGGTGCGGGGATCGCGCAGCACAGCTGTGTGAGCCGGG-----AAGCAGGGC
2370 2380 2390 2400 2410 2420 2430
AAGAGCTCCAGCAACACTGCATATCGGATACACTTACTTTAGCAGCCAGGTTGACAACGTGAGAGGTGCG
2440 2450 2460 2470 2480 2490 2500
ATAGCAAACTGTGAGCAGCGGAAAGTGTAGAGGAAAGTCACTCTCAGCAGCTCTTACATGGGCAT
2510 2520 2530 2540 2550 2560 2570 2580
GATGAGGTGAGCAGGCCCAAGAGGCACTCTCTGGTGTGCCAGTGGGGCCAGGACACTGGTGTGCCCA
2590 2600 2610 2620 2630 2640 2650
GTCAATGGCAGCAGGAGTAGCCAGCAGCCCAAGACTGATCATGAAGCATATAGACAGTAGTAGGCCTG
2660 2670 2680 2690 2700 2710 2720
GCACAGTGTGTGGGTGTCGGGATCCCGAAGAGGTACAGAGCAGGCGCTTCCAGTGGATGAGTGAAGC--ACACTGSCCA
2730 2740 2750 2760 2770 2780 2790
CAGAAATPCCAGACAGCCACAGCCAGGATGAGCAGTGCACCTCAGGGGCGTGGATCGCGCAGCAGCAGC
2800 2810 2820 2830 2840 2850 2860
CCTGCTAGCAGCGCGCCCTTGGATGAGAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
2870 2880 2890 2900 2910 2920 2930
GGCCGGCGGCGGCGCATAGCTCCACGCCAGTGTGCTACTGGCTGAGCTAGGAGGGGACACAGACACGAGCC
2940 2950 2960 2970 2980 2990 3000
CGGNGCCACCGCANNNGAATCCCACTCTTTCCTTACTTACGAGGTTAAGTCAACCCTTNNCTTAC
3010 3020 3030 3040 3050 3060 3070
NCTACTTGAACCTTGTCTNGGCCCAATGAAATTCACCCNACCGGAACCTGATGATCCACTNNCTTCTATAAC
3080 3090 3100 3110 3120 3130 3140
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
3150 3160 3170 3180 3190 3200 3210
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
3220 3230 3240 3250 3260 3270 3280
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
3290 3300 3310 3320 3330 3340 3350
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
3360 3370 3380 3390 3400 3410 3420
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
3430 3440 3450 3460 3470 3480 3490
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
3500 3510 3520 3530 3540 3550 3560
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
3570 3580 3590 3600 3610 3620 3630
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
3640 3650 3660 3670 3680 3690 3700
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
3710 3720 3730 3740 3750 3760 3770
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
3780 3790 3800 3810 3820 3830 3840
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
3850 3860 3870 3880 3890 3900 3910
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
3920 3930 3940 3950 3960 3970 3980
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
3990 4000 4010 4020 4030 4040 4050
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
4060 4070 4080 4090 4100 4110 4120
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
4130 4140 4150 4160 4170 4180 4190
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
4200 4210 4220 4230 4240 4250 4260
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
4270 4280 4290 4300 4310 4320 4330
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
4340 4350 4360 4370 4380 4390 4400
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
4410 4420 4430 4440 4450 4460 4470
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
4480 4490 4500 4510 4520 4530 4540
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
4550 4560 4570 4580 4590 4600 4610
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
4620 4630 4640 4650 4660 4670 4680
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
4690 4700 4710 4720 4730 4740 4750
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
4760 4770 4780 4790 4800 4810 4820
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
4830 4840 4850 4860 4870 4880 4890
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
4900 4910 4920 4930 4940 4950 4960
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
4970 4980 4990 5000 5010 5020 5030
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
5040 5050 5060 5070 5080 5090 5100
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
5110 5120 5130 5140 5150 5160 5170
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
5180 5190 5200 5210 5220 5230 5240
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
5250 5260 5270 5280 5290 5300 5310
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
5320 5330 5340 5350 5360 5370 5380
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
5390 5400 5410 5420 5430 5440 5450
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
5460 5470 5480 5490 5500 5510 5520
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
5530 5540 5550 5560 5570 5580 5590
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
5600 5610 5620 5630 5640 5650 5660
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
5670 5680 5690 5700 5710 5720 5730
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
5740 5750 5760 5770 5780 5790 5800
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
5810 5820 5830 5840 5850 5860 5870
GATGAGGTGAGCAGGCCCAAGAGGCTCAGCAGATGCCCAAGCAGATGCCCAGATGAAG
5880 5890 5900 5910 5920 5930 5940
GATGAGGTGAGCAGGCCCAAG

470 480
AGGGGAGTGGAGTGGGGGAAAC

49. US-09-030-606-110' (1-3410)
US-09-030-747-92 sequence 92. Application US/09020747

Initial Score	=	58	Optimized Score	=	180	Significance	=	0.77
Residue Identity	=	40%	Matches	=	195	Mismatches	=	277
Gaps	=		Conservative Substitutions	=	5		=	0

ACACGGCCACACTGTGGGACAGGCATGTGGACCGGACGCCACAGGGAAGCTGCCACACTGGCCAAATAG

[illegible][illegible]

Residue Identity	=	36%	Matches	=	163	Mismatches	=	280
Gaps	=	19	Conservative Substitutions	=	0			

	X	10	20	30	40
1	T	T	T	T	T
2	T	T	T	T	T
3	T	T	T	T	T
4	T	T	T	T	T
5	T	T	T	T	T
6	T	T	T	T	T
7	T	T	T	T	T
8	T	T	T	T	T
9	T	T	T	T	T
10	T	T	T	T	T
11	T	T	T	T	T
12	T	T	T	T	T
13	T	T	T	T	T
14	T	T	T	T	T
15	T	T	T	T	T
16	T	T	T	T	T
17	T	T	T	T	T
18	T	T	T	T	T
19	T	T	T	T	T
20	T	T	T	T	T
21	T	T	T	T	T
22	T	T	T	T	T
23	T	T	T	T	T
24	T	T	T	T	T
25	T	T	T	T	T
26	T	T	T	T	T
27	T	T	T	T	T
28	T	T	T	T	T
29	T	T	T	T	T
30	T	T	T	T	T
31	T	T	T	T	T
32	T	T	T	T	T
33	T	T	T	T	T
34	T	T	T	T	T
35	T	T	T	T	T
36	T	T	T	T	T
37	T	T	T	T	T
38	T	T	T	T	T
39	T	T	T	T	T
40	T	T	T	T	T
41	T	T	T	T	T
42	T	T	T	T	T
43	T	T	T	T	T
44	T	T	T	T	T
45	T	T	T	T	T
46	T	T	T	T	T
47	T	T	T	T	T
48	T	T	T	T	T
49	T	T	T	T	T
50	T	T	T	T	T
51	T	T	T	T	T
52	T	T	T	T	T
53	T	T	T	T	T
54	T	T	T	T	T
55	T	T	T	T	T
56	T	T	T	T	T
57	T	T	T	T	T
58	T	T	T	T	T
59	T	T	T	T	T
60	T	T	T	T	T
61	T	T	T	T	T
62	T	T	T	T	T
63	T	T	T	T	T
64	T	T	T	T	T
65	T	T	T	T	T
66	T	T	T	T	T
67	T	T	T	T	T
68	T	T	T	T	T
69	T	T	T	T	T
70	T	T	T	T	T
71	T	T	T	T	T
72	T	T	T	T	T
73	T	T	T	T	T
74	T	T	T	T	T
75	T	T	T	T	T
76	T	T	T	T	T
77	T	T	T	T	T
78	T	T	T	T	T
79	T	T	T	T	T
80	T	T	T	T	T
81	T	T	T	T	T
82	T	T	T	T	T
83	T	T	T	T	T
84	T	T	T	T	T
85	T	T	T	T	T
86	T	T	T	T	T
87	T	T	T	T	T
88	T	T	T	T	T
89	T	T	T	T	T
90	T	T	T	T	

[illegible][illegible]

Angle	100	110	120	130	140
80	100	110	120	130	140

ATAAACATTATACTCTGATTGCTCACTTACAGTATAAAATATTTCACCCCGCTAAATATAAATAAGACGACATTT

Year	1950	1951	1952	1953	1954	1955	1956	1957	1958	1959	1960	1961	1962	1963	1964	1965	1966	1967	1968	1969	1970	1971	1972	1973	1974	1975	1976	1977	1978	1979	1980	1981	1982	1983	1984	1985	1986	1987	1988	1989	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																																																																																	
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Year	2020	2021	2022	2023	2024	2025	2026	2027	2028
Population (millions)	7.8	8.1	8.4	8.7	9.0	9.3	9.6	9.9	10.2
GDP (trillion USD)	2.5	2.8	3.1	3.4	3.7	4.0	4.3	4.6	4.9
Life expectancy (years)	75	76	77	78	79	80	81	82	83
Urbanization (%)	55	58	61	64	67	70	73	76	79
Renewable energy share (%)	12	15	18	21	24	27	30	33	36
Digital literacy (%)	45	52	59	66	73	80	87	94	100
Gender inequality index	0.72	0.74	0.76	0.78	0.80	0.82	0.84	0.86	0.88
Carbon footprint (kg CO2e/capita)	1.2	1.3	1.4	1.5	1.6	1.7	1.8	1.9	2.0
Healthcare expenditure (% GDP)	8.5	9.0	9.5	10.0	10.5	11.0	11.5	12.0	12.5
Unemployment rate (%)	6.5	6.8	7.1	7.4	7.7	8.0	8.3	8.6	8.9
Immigration (net, thousands)	150	160	170	180	190	200	210	220	230
Trade share (% GDP)	25	26	27	28	29	30	31	32	33
Research & Development (% GDP)	2.5	2.6	2.7	2.8	2.9	3.0	3.1	3.2	3.3
Public debt (% GDP)	65	68	71	74	77	80	83	86	89
Corruption index	45	48	51	54	57	60	63	66	69
Environmental quality index	60	62	64	66	68	70	72	74	76
Trust in government (%)	55	58	61	64	67	70	73	76	79
Income inequality (Gini index)	35	36	37	38	39	40	41	42	43
Healthcare access (per 1,000 people)	120	125	130	135	140	145	150	155	160
Education expenditure (% GDP)	4.5	4.6	4.7	4.8	4.9	5.0	5.1	5.2	5.3
Infrastructure investment (% GDP)	3.5	3.6	3.7	3.8	3.9	4.0	4.1	4.2	4.3
Foreign aid received (% GDP)	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5	0.5
Disaster risk index	2.5	2.6	2.7	2.8	2.9	3.0	3.1	3.2	3.3
Climate resilience index	30	32	34	36	38	40	42	44	46
Government effectiveness	65	67	69	71	73	75	77	79	81
Business confidence index	50	52	54	56	58	60	62	64	66
Consumer confidence index	40	42	44	46	48	50	52	54	56
Real estate index	70	72	74	76	78	80	82	84	86
Stock market index	12000	12500	13000	13500	14000	14500	15000	15500	16000
Bitcoin price (USD)	15000	16000	17000	18000	19000	20000	21000	22000	23000
Gold price (USD/ounce)	1800	1850	1900	1950	2000	2050	2100	2150	2200
Oil price (USD/barrel)	70	72	74	76	78	80	82	84	86
Wheat price (USD/bushel)	6.0	6.2	6.4	6.6	6.8	7.0	7.2	7.4	7.6
Corn price (USD/bushel)	4.0	4.2	4.4	4.6	4.8	5.0	5.2	5.4	5.6
Soybean price (USD/bushel)	10.0	10.5	11.0	11.5	12.0	12.5	13.0	13.5	14.0
Crude oil price (USD/barrel)	70	72	74	76	78	80	82	84	86
Natural gas price (USD/MMBtu)	3.0	3.2	3.4	3.6	3.8	4.0	4.2	4.4	4.6
Electricity price (USD/kWh)	0.10	0.11	0.12	0.13	0.14	0.15	0.16	0.17	0.18
Propane price (USD/gallon)	2.5	2.6	2.7	2.8	2.9	3.0	3.1	3.2	3.3
Heating oil price (USD/gallon)	3.0	3.1	3.2	3.3	3.4	3.5	3.6	3.7	3.8
Gasoline price (USD/gallon)	2.0	2.1	2.2	2.3	2.4	2.5	2.6	2	

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330 333 336 339 342 345 348 351 354 357 360 363 366 369 372 375 378 381 384 387 390 393 396 399 402 405 408 411 414 417 420 423 426 429 432 435 438 441 444 447 450 453 456 459 462 465 468 471 474 477 480 483 486 489 492 495 498 501 504 507 510 513 516 519 522 525 528 531 534 537 540 543 546 549 552 555 558 561 564 567 570 573 576 579 582 585 588 591 594 597 600 603 606 609 612 615 618 621 624 627 630 633 636 639 642 645 648 651 654 657 660 663 666 669 672 675 678 681 684 687 690 693 696 699 702 705 708 711 714 717 720 723 726 729 732 735 738 741 744 747 750 753 756 759 762 765 768 771 774 777 780 783 786 789 792 795 798 801 804 807 810 813 816 819 822 825 828 831 834 837 840 843 846 849 852 855 858 861 864 867 870 873 876 879 882 885 888 891 894 897 900 903 906 909 912 915 918 921 924 927 930 933 936 939 942 945 948 951 954 957 960 963 966 969 972 975 978 981 984 987 990 993 996 999 1002 1005 1008 1011 1014 1017 1020 1023 1026 1029 1032 1035 1038 1041 1044 1047 1050 1053 1056 1059 1062 1065 1068 1071 1074 1077 1080 1083 1086 1089 1092 1095 1098 1101 1104 1107 1110 1113 1116 1119 1122 1125 1128 1131 1134 1137 1140 1143 1146 1149 1152 1155 1158 1161 1164 1167 1170 1173 1176 1179 1182 1185 1188 1191 1194 1197 1200 1203 1206 1209 1212 1215 1218 1221 1224 1227 1230 1233 1236 1239 1242 1245 1248 1251 1254 1257 1260 1263 1266 1269 1272 1275 1278 1281 1284 1287 1290 1293 1296 1299 1302 1305 1308 1311 1314 1317 1320 1323 1326 1329 1332 1335 1338 1341 1344 1347 1350 1353 1356 1359 1362 1365 1368 1371 1374 1377 1380 1383 1386 1389 1392 1395 1398 1401 1404 1407 1410 1413 1416 1419 1422 1425 1428 1431 1434 1437 1440 1443 1446 1449 1452 1455 1458 1461 1464 1467 1470 1473 1476 1479 1482 1485 1488 1491 1494 1497 1500 1503 1506 1509 1512 1515 1518 1521 1524 1527 1530 1533 1536 1539 1542 1545 1548 1551 1554 1557 1560 1563 1566 1569 1572 1575 1578 1581 1584 1587 1590 1593 1596 1599 1602 1605 1608 1611 1614 1617 1620 1623 1626 1629 1632 1635 1638 1641 1644 1647 1650 1653 1656 1659 1662 1665 1668 1671 1674 1677 1680 1683 1686 1689 1692 1695 1698 1701 1704 1707 1710 1713 1716 1719 1722 1725 1728 1731 1734 1737 1740 1743 1746 1749 1752 1755 1758 1761 1764 1767 1770 1773 1776 1779 1782 1785 1788 1791 1794 1797 1800 1803 1806 1809 1812 1815 1818 1821 1824 1827 1830 1833 1836 1839 1842 1845 1848 1851 1854 1857 1860 1863 1866 1869 1872 1875 1878 1881 1884 1887 1890 1893 1896 1899 1902 1905 1908 1911 1914 1917 1920 1923 1926 1929 1932 1935 1938 1941 1944 1947 1950 1953 1956 1959 1962 1965 1968 1971 1974 1977 1980 1983 1986 1989 1992 1995 1998 2001 2004 2007 2010 2013 2016 2019 2022 2025 2028 2031 2034 2037 2040 2043 2046 2049 2052 2055 2058 2061 2064 2067 2070 2073 2076 2079 2082 2085 2088 2091 2094 2097 2100 2103 2106 2109 2112 2115 2118 2121 2124 2127 2130 2133 2136 2139 2142 2145 2148 2151 2154 2157 2160 2163 2166 2169 2172 2175 2178 2181 2184 2187 2190 2193 2196 2199 2202 2205 2208 2211 2214 2217 2220 2223 2226 2229 2232 2235 2238 2241 2244 2247 2250 2253 2256 2259 2262 2265 2268 2271 2274 2277 2280 2283 2286 2289 2292 2295 2298 2301 2304 2307 2310 2313 2316 2319 2322 2325 2328 2331 2334 2337 2340 2343 2346 2349 2352 2355 2358 2361 2364 2367 2370 2373 2376 2379 2382 2385 2388 2391 2394 2397 2400 2403 2406 2409 2412 2415 2418 2421 2424 2427 2430 2433 2436 2439 2442 2445 2448 2451 2454 2457 2460 2463 2466 2469 2472 2475 2478 2481 2484 2487 2490 2493 2496 2499 2502 2505 2508 2511 2514 2517 2520 2523 2526 2529 2532 2535 2538 2541 2544 2547 2550 2553 2556 2559 2562 2565 2568 2571 2574 2577 2580 2583 2586 2589 2592 2595 2598 2601 2604 2607 2610 2613 2616 2619 2622 2625 2628 2631 2634 2637 2640 2643 2646 2649 2652 2655 2658 2661 2664 2667 2670 2673 2676 2679 2682 2685 2688 2691 2694 2697 2700 2703 2706 2709 2712 2715 2718 2721 2724 2727 2730 2733 2736 2739 2742 2745 2748 2751 2754 2757 2760 2763 2766 2769 2772 2775 2778 2781 2784 2787 2790 2793 2796 2799 2802 2805 2808 2811 2814 2817 2820 2823 2826 2829 2832 2835 2838 2841 2844 2847 2850 2853 2856 2859 2862 2865 2868 2871 2874 2877 2880 2883 2886 2889 2892 2895 2898 2901 2904 2907 2910 2913 2916 291

AGCTGATATNTGAGCGGAAGANTAGCCTTTCTACTTCACAGACACAACTCCCTTCATATTTGGGAGTGA

GGGGT AGGGG AAAAG TTGGGG GTAGGGG AATTT TGGG CAGTGCCTT CATCAG CCCCAGT CCTTAG AGAGAGTAC

NAAAGTTATGTCTCTTACAGATGGGATGCTTTTGTGGCAATTCTG
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50. US-09-030-606-110' (1-3410)

Initial Score	=	58	Optimized Score	=	253	Significance	=	0.77
Residue Identity	=	38%	Matches	=	304	Mismatches	=	451
			Conservative Substitutions	=	45		=	0

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[illegible]

[illegible]

170 X 180 190 200 210 220
 GCTAAATAAATAAGACGACATTATTGCAACGSCACTTAAACCCCCCTGAGAGATAAG
 CACTCTTGT
 490

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62.  US-09-030-606-110' (1-3410)
    US-09-020-747-52 Sequence 52, Application US/09020747
Initial Score      = 55 Optimized Score = 72 Significance = 0.65
Residue Identity  = 41% Matches      = 72 Mismatches = 103
Gaps              = 0 Conservative Substitutions = 0

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[illegible]

170 X 180 190 200 210 220
GCTAAATAAATAGACGACATTATTGAAACGCACTTAACCCGCCCTGAGAGATAAG
CACTCTTGT
400

63. US-09-030-606-110' (1-3410)
US-09-020-747-10 Sequence 103, Application US/09020747

Initial Score	=	55	Optimized Score	=	201	Significance	=	0.65
Residue Identity	=	36%	Matches	=	223	Mismatches	=	358

GCCTCTGCTGATGCTCTCGTACGTGTGGTGGTGAGCCACCGAGCGGTGTTCCGGCCGG
500 510 520 530 540 550 560
1630 1640 1650 1660 1670 1680 1690
GACAGCAGGAAGGCACTATCCAGGATGGCGAGTCCAGGAGATGCCCGCGCGGACCACTGGCTCG
1700 1710 1720 1730 1740 1750 1760
GTGGCTCACCCACACACAGTACCGAGACATCACAGGACAGGCCCCCGACAGCGGGTGAGTGGG
1770 1780 1790 1800 1810 1820
A-----GCAGGCCACTGCGCTCCAGCACCCACCGTGTCCATTAGGAGGAGCTCCAGGCTTAGG
ATTTACTTTGCTACACAGAGTAGTATTTGACAAGAGCGACTTGGCCAAATACTACAGCTAGAAAACCTTCCAGC
710 720 730 740 750 760 770 780
1830 1840 1850 1860 1870 1880 1890
GCCT--GCGAGGAGCTGGTCATCAGGCTGCTCTCACTGCTAGCACCTTCCAGTCTCCCTCGTATTGGGC
1900 1910 1920 1930 1940 1950 1960
ACATTGGGTGGAGGGCTGCTCTCACTGGGTCCAGCTCCCGCTCCT-GTATAGCCCATGGGCTCGCGGG
790 800 810 820 830 840 850
1970 1980 1990 2000 2010 2020 2030
AGGAACACCTGCTTCTCCGGTGTAGAGGAGGCCAGTGTGTAGG-----CAGGATCTGACGGCTGAGNA
2040 2050 2060 2070 2080 2090 2100
GGTCAACCCGCTGAGCGGCTGAGCTGTACACACGCGCACACTGTGGACAGCATGTGGCACCGCAGC
2110 2120 2130 2140 2150 2160 2170
GCTCA--CAGTGGGGCTGGGGCTCCCTCTCTCTC--TCTCCCACTCTCTAGGGTGTCTGACTGAGGC
930 940 950 960 970 980 990
2180 2190 2200 2210 2220 2230 2240 2250
CAGAGAGAAGACCCAGGAGATGGCGCACTGCAGCAAGACCCAGGCTGCCATCCGAGCCCTCATCAT
2260 2270 2280 2290 2300 2310 2320
GTAACAGAGCTGAAGTCTATGAGTCCATCCAGCTGCACAGCTCAGCCAGAGAGCGCGCAGGCTGG
2330 2340 2350 2360 2370 2380 2390
GGGCATCGCGCAGCACAGCTGGTGCACCGGGAGCAGGCGCCAGGTTCGCGAAGCAAGCGGCGCG
2400 2410 2420 2430 2440 2450 2460
TTATGTAGCTTTGCATGGAGTTTCTAGGATGAACACTCTCTCCATGGGATTTGAACATATAAGTTAT
1210 1220 1230 1240 1250 1260 1270
2470 2480 2490 2500 2510 2520 2530
CTCTCAGCCACCAAGCATGTGGCTGTACGCAAGTGGAGAGATGAGGTGAGGCAAGGACACTC
2540 2550 2560 2570 2580 2590 2600 2610
CTCTGGTGGCCAGTGGGGCCAGGCACTGTCTCCAGTCAATGCGCAGCAGGAGTACCCAGCA
2620 2630 2640 2650 2660 2670 2680
GCCCCCAAGACTGATGATGAGGCGATAGACAGACTAGGCTGGCGAGAGTGTCCGGTCCCGAAGAGTTC
2690 2700 2710 2720 2730 2740 2750
AGAGAGAGGCGCTCCAGTGGAGTGAAGCACACCTGGCCACAGAGTCCAGCAGCCCGCAGCATGAG
2760 2770 2780 2790 2800 2810 2820
CAGTGGCAGCTCCAGGCGCTGGGATCGGCGCAGCAGGCGCTCTAGCCAGCGGCTTGGGATGAGAA
2830 2840 2850 2860 2870 2880 2890
GAGCTCAGCAGGATGCCAAGACAGTCCACATGAAGCGCGCGGCGCCATAGCGTCCACGCGCAGTG
2900 2910 2920 2930 2940 2950 2960 2970
GTCACTGGCTGAGCTAGGAGCGGACACAGACAGCCAGCGCTGACCAATGCCCAGCAGGCTGTCAT
2980 2990 3000 3010 3020 3030 3040
GAACCTCTCTCTTACCCCACTTCCAGCAGCAGGCGGACATAGTGTGCTGCGCGGCAACACACCTC
3050 3060 3070 3080 3090 3100 3110
CAGGCCAAAGTTAGCAGGTTGACAGCAAGAGTGGGCTTTCGGTGGCCGACAGGCGGCTCACCCACAG
3120 3130 3140 3150 3160 3170 3180
CCTCTGGACCATAGTGGGCCAGGCGGTAGGCTCAGGGCGGCTTCCAGGCACTCCAGAACTGCTGCTC
3190 3200 3210 3220 3230 3240 3250
GGCTCTGCTCCAGAGCTGGCGCTCTCTCTGCTGGCCCAACTGCCCTAGGAATCAGCCAGGCGGCCAT
3260 3270 3280 3290 3300 3310 3320
GTTTATGCTGACAAATTAAGGCTTCTTATATATTTA
2120 2130 2140 2150 X
TTCTGCCAGCCCTTTGG

GTATCCACCCCTCTTACCTTTTATCAGGATGTGG-----CTGTGGTCTCTTGTGTCATCACAGA
1350 1360 1370 1380 1390 1400 1410
2470 2480 2490 2500 2510 2520 2530
CTCTCAGCCACCAAGCATGTGGCTGTACGCAAGTGGAGAGATGAGGTGAGGCAAGGACACTC
1420 1430 1440 1450 1460 1470 1480
GACACAGCATTTAAATTAACCT--TATTTATTAAACAAAGTAGAGG--GAATCCATGTAGCTTTT
1490 1500 1510 1520 1530 1540 1550
2540 2550 2560 2570 2580 2590 2600 2610
CTCTGGTGGCCAGTGGGGCCAGGCACTGTCTCCAGTCAATGCGCAGCAGGAGTACCCAGCA
2620 2630 2640 2650 2660 2670 2680
GCCCCCAAGACTGATGATGAGGCGATAGACAGACTAGGCTGGCGAGAGTGTCCGGTCCCGAAGAGTTC
2690 2700 2710 2720 2730 2740 2750
AGAGAGAGGCGCTCCAGTGGAGTGAAGCACACCTGGCCACAGAGTCCAGCAGCCCGCAGCATGAG
2760 2770 2780 2790 2800 2810 2820
CAGTGGCAGCTCCAGGCGCTGGGATCGGCGCAGCAGGCGCTCTAGCCAGCGGCTTGGGATGAGAA
2830 2840 2850 2860 2870 2880 2890
GAGCTCAGCAGGATGCCAAGACAGTCCACATGAAGCGCGCGGCGCCATAGCGTCCACGCGCAGTG
2900 2910 2920 2930 2940 2950 2960 2970
GTCACTGGCTGAGCTAGGAGCGGACACAGACAGCCAGCGCTGACCAATGCCCAGCAGGCTGTCAT
2980 2990 3000 3010 3020 3030 3040
GAACCTCTCTCTTACCCCACTTCCAGCAGCAGGCGGACATAGTGTGCTGCGCGGCAACACACCTC
3050 3060 3070 3080 3090 3100 3110
CAGGCCAAAGTTAGCAGGTTGACAGCAAGAGTGGGCTTTCGGTGGCCGACAGGCGGCTCACCCACAG
3120 3130 3140 3150 3160 3170 3180
CCTCTGGACCATAGTGGGCCAGGCGGTAGGCTCAGGGCGGCTTCCAGGCACTCCAGAACTGCTGCTC
3190 3200 3210 3220 3230 3240 3250
GGCTCTGCTCCAGAGCTGGCGCTCTCTCTGCTGGCCCAACTGCCCTAGGAATCAGCCAGGCGGCCAT
3260 3270 3280 3290 3300 3310 3320
GTTTATGCTGACAAATTAAGGCTTCTTATATATTTA
2120 2130 2140 2150 X
TTCTGCCAGCCCTTTGG

A-----CGAGCCACTGCCTCCAGCAGCCACCGCTGCTTCTAGGAAAGGGAGCTCCAGGCTTAGG
1780 1790 1800
ATTTACTTGTACACAGGTAGTATTTGACAAGAGCGACTTGGCCAAATACTACGCGTAGAAAACTTCCACGC
710 720 730 740 750 760 770 780
1830 1840 1850 1860 1870 1880 1890
GCCT--GGCAGGAAGCTGGTCATCAGGCTGTCTCTACATGCTAGCAGCTCCAGTGTCCCTCGGTATTTGGGC
1900 1910 1920 1930 1940 1950 1960
AGGAACACCTGTCTTCCCGGTGGTAGAGGAGGCCAGTGTGTAGG---CAGGATCTGCAGGCTCAGAAA
CTGCGCGCCAGTTCTGTGTCTGCCAAAGTAAATGGCTCTCTCTGCTGCCACCTGTGTCTCTGAGGTGGTA
860 870 880 890 900 910 920
ACATTGGGTGGAGGCGCTGCCTACTGGGTCCCGAGCTCCCGCTCCT-GTTAGCCCNATGGGCTGCCGG
790 800 810 820 830 840 850
1970 1980 1990 2000 2010 2020 2030
GGTGAACCCGGTCAGGCGCGCTGAAGCTGTCCACCAGCCGACACTGTGGGACAGGCAATGGCAGCCGCGCAGC
GCTGCA-CAGCTGGGGGCTGGGCGCTCCCTCTCCTC--TCTCCCACTCTTAGGCTCGCTGACTGGAGGC
930 940 950 960 970 980 990
2040 2050 2060 2070 2080 2090 2100
CACAGGAAAGCTGCCACACTGCCAAATAGACTCTCGAGTGCAGGCTGCTGACAGGCGGTCCATGAC
CTTCCAGGGGTTTCAGTCTGAGCTTATACAGGAGGCCAAGAGGCTCCATGCTCACTGGAATG-----
1000 1010 1020 1030 1040 1050
2110 2120 2130 2140 2150 2160 2170
CAGAGAAGAACCCAGGAGATGGCGACTGTCAGGAACAGCCCCAGGCTGCCATTCGAGCGCTTCATCATTA
CGGGACTCTGCAAGTGTGATTACCCAGGCTCAGGCTTAACAGCTAGCTCTCTAGTTGAGACACACCTTAGAGA
1060 1070 1080 1090 1100 1110 1120
2180 2190 2200 2210 2220 2230 2240 2250
GTGTCTCCGGGCTTCGGTGCCTGGCTCAGCTCTGGCAGCGCTGTGTACAGCCCTCGCCACCAAGAAATCCGT
AGGGTTTGTGGAGCTGAATAAATCAGTCACTGTGTTCCCACTCTTAAGCGCCCTTAACTCGACGCTTCGT
1130 1140 1150 1160 1170 1180 1190 1200
GTAAACAGCGTGAAGTCTAGTGCCTCCAGCTGCACAGCTCAGCCAGGAAGCCGCGCAGGCTGCG
TTAATGTAGTCTTGCATGGAGGTTTCTAGGATGAACAACTCCTCCATGGGTTTGAACATATGAAAGTTAT
1210 1220 1230 1240 1250 1260 1270
2260 2270 2280 2290 2300 2310 2320
GTAAACAGCGTGAAGTCTAGTGCCTCCAGCTGCACAGCTCAGCCAGGAAGCCGCGCAGGCTGCG
GGCAGTCGGCAGCAGCTGTGTACAGCCGGGAGCAGGGCGCCAGGTTCCGGAAGCAAGCGGGCGCG
TTGTAGGGAAGAGTCTCTGAGGGCAACACAGAACCAGGTCCCTCAGCCACAGCA-TGTCTTTTTCG
1280 1290 1300 1310 1320 1330 1340
2330 2340 2350 2360 2370 2380 2390
GATGACAGCAGTGGGGCGACAAGAGGGCGCCAGACCCCTTCGTGTGCTCGGTGGGCCCCAGCGCTGC
TGATCCACCCCTCTTACCTTTTATCAGGATGTGG-----CTGTGTGTCCTCTGTTGCCCATCAGACA
1350 1360 1370 1380 1390 1400 1410
2400 2410 2420 2430 2440 2450 2460
GCATGACAGCAGTGGGGCGACAAGAGGGCGCCAGACCCCTTCGTGTGCTCGGTGGGCCCCAGCGCTGC
TGATCCACCCCTCTTACCTTTTATCAGGATGTGG-----CTGTGTGTCCTCTGTTGCCCATCAGACA
1420 1430 1440 1450 1460 1470
2470 2480 2490 2500 2510 2520 2530
CTCTCTCAGCCACCGACGTGTGGTGTCTAGCGAGGTGAGGAAGTAGGCTGACAGGCCAAGAGGACCTC
GACACAGGCAATTAATATTAACT--TATTATTAAACAAGATGAAG---GAATCCATTTGCTAGCTTTT
1480 1490 1500 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600
2540 2550 2560 2570 2580 2590 2600 2610
CTCCTGGGTGCCAGGTAGGGGCCAGCTGCTGCCAGTCAATGCGAGGAGGAGGTAGCCACAGCA
CTGTGTGTGTCTAATATTGGGTAGGTGGGGATCCCCACAATCAGGTCCCTGAGATG-CTGTCTA
1480 1490 1500 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600
2620 2630 2640 2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760 2770 2780 2790 2800 2810 2820 2830 2840 2850 2860 2870 2880 2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990 3000

[illegible]

80. US-09-030-606-110' (1-3410) Application US/08850713

US-08-850-713-16 sequence 107, approximately 1000 bp

Initial score	=	54	Optimized score	=	835
Residue Identity	=	37%	Matches	=	Substitutions

Gaps - 83 Conservative substitutions 1000

980 990 1000 1010 1020 1030 1040
mmcAAATCCCATGGAGGAGCTGTTTCATCCCTAGAAACTCCCATGCAAGAGCTACATTAAACGAAGCTGCAGGT

IICNNCCCCGCGGGCTTACAGGGCCGTGCC

80

10. x

1050
1060
1070
1080
1090
1100
1110

TAAGGGGCTTAGAGATGGGAACACAGGTGACTGAGTTTATTCACGTCCTCCGAGGAGGCTT

AGAGCTGAGCCGGGACCGCAGGCCCGGAGAC--ACTATGATGAAGGGGTTCGGATGGGCACGCG

	1190	1180	1170	1160	1150	1140	1130	1120	1110	1100	1090	1080	1070	1060	1050	1040	1030	1020	1010	1000	990	980	970	960	950	940	930	920	910	900	890	880	870	860	850	840	830	820	810	800	790	780	770	760	750	740	730	720	710	700	690	680	670	660	650	640	630	620	610	600	590	580	570	560	550	540	530	520	510	500	490	480	470	460	450	440	430	420	410	400	390	380	370	360	350	340	330	320	310	300	290	280	270	260	250	240	230	220	210	200	190	180	170	160	150	140	130	120	110	100	90	80	70	60	50	40	30	20	10	0
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1120 TCAACTAGGAGGCTGTTACCCCTGAGCCTGGTAAATCCACCTGCAGAGTCCCCCGCATTCGATAT
1130
1140
1150

TCCTTGCAGTGGGCCATCTCCCTGGTCTTCTCTCTGGTTCATGGACCGCTGGTGAGCGCATTCGGCATTCCGAC

	100	110	120	130	140	150	160
--	-----	-----	-----	-----	-----	-----	-----

1200 1210 1220 1230 1240 1250 1260

GAGCCCTTCGCGCCGCCGCCTGGTGGTGCGCGGT-----GCCACATGCCTGTCCCACAGTT

CAGTCTATTGGCCAGTGCGGCAATTCGGC
170 180 190 200 210 220

1270 1280 1290 1300 1310 1320 1330

us-09-030-606-110-inv.res

TGC - GGTTC	1910	1920	1930	1940	1950	1960	1970
3050	3060	3070	3080	3090	3100	3110	•
CCAAAGGTTAGCAGGTTGACCAAGAGCTGGGCTTTCCGGTCGCCGAGCAGCGGCTCACCCACAGCCTC							
CTCAGGAGCACCCCTGCCTGCCTGAGCTAAGGAGGCTCT - - - - ATCTCTCAGGGGGGTTTAAGTGCCCTTTGC							
1980	1990	2000	2010	2020	2030	2040	
3120	3130	3140	3150	3160	3170	3180	3190
TGGACCATAGTTGGCGCAGCGGCTAGGGCTCAGGGGGCGGTTCAGGCACTCCAGAACTGCTCGTCTCGGCT							
AAATACTCGTCTATTATTATTAGCGGGGTGAATATTATACCTAGTCAGCAACAGAGTAAATAGTTT							
2050	2060	2070	2080	2090	2100	2110	
3200	3210	3220	3230	3240	3250	3260	
CTGCTCAGAAGCTGGCGCTTCCTCTGCTGCGGCCAACTGCCTAGGAATCAGCCAGCGGCCCACTTCT							
ATGGTGACAANAATTAAAGGCTTCTTATATAGTTTATGG							
2120	2130	2140	2150	x			
3270	3280						
GCCAGCCCTTTGGTGCC							

> O < IntelliGenetics
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-030-606-173.res made by tport on Thu 1 May 103 14:56:34-PDT.

Query sequence being compared:US-09-030-606-173 (1-1265)
Number of sequences searched: 410
Number of scores above cutoff: 410

Results of the initial comparison of US-09-030-606-173 (1-1265) with:

File : 6130043.seq
File : 6252047.seq
File : US08806596.seq
File : US08850713.seq
File : US08904809.seq
File : US09020747.seq
File : US09841894A.seq

1000-

N

U 500-

M

B

E

R

O

F 100* *

S

E 50-

Q

U

E

N

C

E

S

SCORE 0

STDEV 0

Similarity matrix

Mismatch penalty

Gap penalty

Gap size penalty

Cutoff score

Randomization group

Scores:

Mean

Median

Standard Deviation

63.84

Times: CPU 00:00:01.00
Total Elapsed 00:00:01.00

Number of residues: 189792
Number of sequences searched: 410
Number of scores above cutoff: 410

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was found:

Sequence Name	Description	Length	Score	Init. Opt.
1. US-09-020-747-17	Sequence 173, Application	1265	1265	1265

The list of other best scores is:

Sequence Name	Description	Length	Score	Init. Opt.
2. US-09-020-747-17	Sequence 171, Application	1248	803	1130
3. US-09-020-747-17	Sequence 175, Application	1167	790	1112
4. US-09-020-747-17	Sequence 174, Application	1459	529	688
5. US-09-020-747-17	Sequence 177, Application	1119	482	597
6. US-08-904-809-45	Sequence 45, Application	234	155	204
7. US-09-020-747-45	Sequence 45, Application	234	155	204
8. US-08-806-596-23	Sequence 23, Application	872	93	240
9. US-09-020-747-10	Sequence 109, Application	1524	89	444
10. US-08-806-596-16	Sequence 16, Application	801	84	268
11. US-08-904-809-16	Sequence 16, Application	801	84	268
12. US-09-020-747-16	Sequence 16, Application	801	84	268
13. US-08-904-809-8	Sequence 8, Application	799	76	252
14. US-09-020-747-13	Sequence 136, Application	399	70	130
15. US-08-904-809-69	Sequence 69, Application	536	69	185
16. US-09-020-747-69	Sequence 69, Application	536	69	185
17. US-09-020-747-40	Sequence 40, Application	753	67	249
18. US-08-806-596-3	Sequence 3, Application	773	65	263
19. US-09-020-747-3	Sequence 3, Application	773	65	263
20. US-08-904-809-32	Sequence 32, Application	789	65	255
21. US-09-020-747-84	Sequence 84, Application	380	64	125
22. US-09-020-747-21	Sequence 21, Application	755	63	209
23. US-08-806-596-38	Sequence 38, Application	724	62	208
24. US-09-020-747-11	Sequence 110, Application	3410	62	437
25. US-08-904-809-36	Sequence 36, Application	814	60	253
26. US-09-020-747-36	Sequence 36, Application	814	60	253
27. US-09-020-747-16	Sequence 160, Application	380	59	126
28. US-08-904-809-40	Sequence 40, Application	753	59	249
29. US-08-806-596-26	Sequence 26, Application	820	59	197
30. US-08-904-809-66	Sequence 66, Application	305	58	115
31. US-09-020-747-66	Sequence 66, Application	305	58	115
32. US-08-806-596-17	Sequence 17, Application	740	57	250
33. US-08-904-809-17	Sequence 17, Application	740	57	250
34. US-09-020-747-17	Sequence 17, Application	740	57	250
35. US-09-020-747-11	Sequence 111, Application	1289	57	429
36. US-08-806-596-13	Sequence 13, Application	729	56	251
37. US-08-904-809-13	Sequence 13, Application	729	56	251
38. US-09-020-747-13	Sequence 13, Application	729	56	251
39. US-08-806-596-40	Sequence 40, Application	753	56	249
40. US-08-904-809-21	Sequence 21, Application	755	56	209
41. US-09-020-747-26	Sequence 26, Application	820	56	239
42. US-09-020-747-94	Sequence 94, Application	495	55	162
43. US-08-904-809-26	Sequence 26, Application	820	55	239
44. US-09-020-747-15	Sequence 153, Application	285	54	96
45. US-09-020-747-31	Sequence 31, Application	799	54	268

1. US-09-030-606-173 (1-1265)
 US-09-020-747-17 Sequence 173, Application US/09020747
 Initial Score = 1265 Optimized Score = 1265 Significance = 19.27
 Residue Identity = 100% Matches = 1265 Mismatches = 0
 Gaps = 0 Conservative Substitutions = 0

X 10 20 30 40 50 60 70
 GGCAGCCGACATCGCAGCCCTGGCAGGCGGCACTGGTATGGAACCAATGTTCTGCTCGGCGCTCTG
 GGCAGCCGACATCGCAGCCCTGGCAGGCGGCACTGGTATGGAACCAATGTTCTGCTCGGCGCTCTG
 X 10 20 30 40 50 60 70

80 90 100 110 120 130 140
 GTGCATCCGAGTGGGTGTGTCAGCGGCACACTGTTTCAGAACTCTTACACCATCGGGCTGGGCTGCAC
 GTGCATCCGAGTGGGTGTGTCAGCGGCACACTGTTTCAGAACTCTTACACCATCGGGCTGGGCTGCAC
 80 90 100 110 120 130 140

150 160 170 180 190 200 210
 AGTCTTGAAGCCGACCAAGAGCAGGAGCCAGATGGTGGAGGCCAGCTCTCCGTACGGCACCAGAGTAC
 AGTCTTGAAGCCGACCAAGAGCAGGAGCCAGATGGTGGAGGCCAGCTCTCCGTACGGCACCAGAGTAC
 150 160 170 180 190 200 210

220 230 240 250 260 270 280
 AACAGACCTTGTCTGCTTACGACCTCATCTCAAGTTGACGAATCCGCTCCGAGTCTGACACCATC
 AACAGACCTTGTCTGCTTACGACCTCATCTCAAGTTGACGAATCCGCTCCGAGTCTGACACCATC
 220 230 240 250 260 270 280

290 300 310 320 330 340 350 360
 CCGAGCATCAGCATGTTGGCAGTGGCCCTACCGCGGGAACCTTCCCTGCTGCTGGGCTGCTG
 CCGAGCATCAGCATGTTGGCAGTGGCCCTACCGCGGGAACCTTCCCTGCTGCTGGGCTGCTG
 290 300 310 320 330 340 350 360

370 380 390 400 410 420 430
 CGGACGTTGAGTTCAGGCTGCTGCTCCCTTCAAGAGGAGTCTCTGCCAGTGTGCTGCTGAGG
 CGGACGTTGAGTTCAGGCTGCTGCTCCCTTCAAGAGGAGTCTCTGCCAGTGTGCTGCTGAGG
 370 380 390 400 410 420 430

440 450 460 470 480 490 500
 CAGAGCTCTGCTGCCAGGAGATGCTACCGGTGCTGAGTGGTCAAGTGTGCTGCTGCTGAGG
 CAGAGCTCTGCTGCCAGGAGATGCTACCGGTGCTGAGTGGTCAAGTGTGCTGCTGCTGAGG
 440 450 460 470 480 490 500

510 520 530 540 550 560 570
 TCTGAGTAAGTCTATGACCGCTGTACACCCAGCATGTTCTGCGCGGCGGAGGCAAGACCAAGAG
 TCTGAGTAAGTCTATGACCGCTGTACACCCAGCATGTTCTGCGCGGCGGAGGCAAGACCAAGAG
 510 520 530 540 550 560 570

580 590 600 610 620 630 640
 ACTCTGCAACGGTGACTCTGGGGGCGCCCTGATCTGCAACGGGTACTTGCAGGGCCCTTGTCTTCGGAA
 ACTCTGCAACGGTGACTCTGGGGGCGCCCTGATCTGCAACGGGTACTTGCAGGGCCCTTGTCTTCGGAA
 580 590 600 610 620 630 640

650 660 670 680 690 700 710 720
 AAGCCCGTGTGGCCAGTGTGGCGTGGCAGTGTCTACCAACCTCTGCAAAATTCAGTGGATAGAGA
 AAGCCCGTGTGGCCAGTGTGGCGTGGCAGTGTCTACCAACCTCTGCAAAATTCAGTGGATAGAGA
 650 660 670 680 690 700 710 720

730 740 750 760 770 780 790
 AAACCGTCCAGGCCAGTTAACTCTGGGACTGGGAACCCATGAAATGACCCCAATACATCTCGGGAG
 AAACCGTCCAGGCCAGTTAACTCTGGGACTGGGAACCCATGAAATGACCCCAATACATCTCGGGAG
 730 740 750 760 770 780 790

2. US-09-030-606-173 (1-1265)

US-09-020-747-17 Sequence 171, Application US/09020747

Initial Score = 803 Optimized Score = 1130 Significance = 12.03
 Residue Identity = 91% Matches = 1163 Mismatches = 19
 Gaps = 95 Conservative Substitutions = 0

X 10 20 30 40
 GGCAGCCCAATCATATAAAGCGGAGGAGTGCAGCCGCACTCGCAGCGGCACTGGTATGGA
 GGCAGCCCAATCATATAAAGCGGAGGAGTGCAGCCGCACTCGCAGCGGCACTGGTATGGA
 10 20 30 40 50 60 70

50 60 70 80 90 100 110
 AACGAATGTTGCTGCGGGGCTCTGCTGTCATCCGAGTGGTGTGTGTCAGCCGACACTGTTCCAGAA
 AACGAATGTTGCTGCGGGGCTCTGCTGTCATCCGAGTGGTGTGTGTCAGCCGACACTGTTCCAGAA
 50 60 70 80 90 100 110

120 130 140 150 160 170
 -----CTCCTACACATCGGCTGGGCTGCACAGTCTTCCAGCCGACCAAGAGGAGGAGCAG
 TGAGTCAGAGCTCTCTACACATCGGCTGGGCTGCACAGTCTTCCAGCCGACCAAGAGGAGCAG
 120 130 140 150 160 170

180 190 200 210 220 230 240
 ATGTGGAGGCCAGCTCTCTCGTACGGCACCAGAGTACACAGACCTTGTCTGCTAAGACCTCATGCTC
 ATGTGGAGGCCAGCTCTCTCGTACGGCACCAGAGTACACAGACCTTGTCTGCTAAGACCTCATGCTC
 180 190 200 210 220 230 240

220 230 240 250 260 270 280

250 260 270 280 290 300 310 320
ATCAAGTTGGACGAATCCGTTCTCCGAGTCTGACACCATCCGGAGCATCAGCATTGCTTCGCAGTCCCTAC
ATCAAGTTGGACGAATCCGTTCTCCGAGTCTGACACCATCCGGAGCATCAGCATTGCTTCGCAGTCCCTAC
290 300 310 320 330 340 350 360
CGCGGGAACCTTGCCTGTTCTTGCGTGGGCTGCTGGCGAACGTGAGCTCACGGGTGTGTGTCTGCGCC
CGCGGGAACCTTGCCTGTTCTTGCGTGGGCTGCTGGCGAAC
370 380 390 400
TCTTCAAGGAGTCTCTGCCAGTCTCGGGGGGCTGACCACGAGCTCTGCGTCCCGAGAGAAATGCCTACCG
-----GGCAGAAATGCCCTACCG
410 420 430 440 450 460
TGCTGCAGTGGCTCAACGTGTCCGTGTGTCTGAGGAGTCTGCAGTAAGCTCTATCACCGCTGTATACCACC
TGCTGCAGTGGCTCAACGTGTCCGTGTGTCTGAGGAGTCTGCAGTAAGCTCTATCACCGCTGTATACCACC
430 440 450 460 470 480 490
540 550 560 570 580 590 600
CCAGCATGTTCTGCGCGCGGAGGCAAGACCAAGAGGACTCTGCAACGGTGACTCTGGGGGGCCCTGTA
CCAGCATGTTCTGCGCGCGGAGGCAAGACCAAGAGGACTCTGCAACGGTGACTCTGGGGGGCCCTGTA
500 510 520 530 540 550 560
610 620 630 640 650 660 670 680
TCTGCAACGGGTACTTGCAGGGCTTGTGTCTTCGGAAGCCCGTGTGGCCAAAGTTGCGGTGCCAGTGG
TCTGCAACGGGTACTTGCAGGGCTTGTGTCTTCGGAAGCCCGTGTGGCCAAAGTTGCGGTGCCAGTGG
570 580 590 600 610 620 630
TCTACCAACCTCTGCAAAATTCAGTGAGTGATAGAGAAACCGTCCAGGCCAGTTAACTCTGGGGAGCTGG
640 650 660 670 680 690 700
TCTACCAACCTCTGCAAAATTCAGTGAGTGATAGAGAAACCGTCCAGGCCAGTTAACTCTGGGGAGCTGG
760 770 780 790 800 810 820
GAACCCATGAAATTCAGCCCGCCCAATACATCTCGGGGAAGAAATTCAGGAATATCTGTTCAGCCAGCCCTCTC
GAACCCATGAAATTCAGCCCGCCCAATACATCTCGGGGAAGAAATTCAGGAATATCTGTTCAGCCAGCCCTCTC
710 720 730 740 750 760 770 780 790
830 840 850 860 870 880 890
CCTCAGGCCAGGAGTCCAGGCCCGCCAGCCCTCTCCTCCTCAACACCAAGGTACAGATCCCGAGCCCTCTC
CCTCAGGCCAGGAGTCCAGGCCCGCCAGCCCTCTCCTCCTCAACACCAAGGTACAGATCCCGAGCCCTCTC
790 800 810 820 830 840 850
900 910 920 930 940 950 960
CCCTCAGACCAGAGTCCAGGCCCGCCAGCCCTCTCCTCCTCAGACCAGGAGTCCAGCCCTCTCCTCCTC
CCCTCAGACCAGAGTCCAGGCCCGCCAGCCCTCTCCTCCTCAGACCAGGAGTCCAGCCCTCTCCTCCTC
860 870 880 890 900 910 920
970 980 990 1000 1010 1020 1030 1040
AGACCCAGGAGTCCAGGCCCGCCAGCCCTCTCCTCCTCAGACCAGGAGTCCAGCCCTCTCCTCCTC
AGACCCAGGAGTCCAGGCCCGCCAGCCCTCTCCTCCTCAGACCAGGAGTCCAGCCCTCTCCTCCTC
930 940 950 960 970 980 990
1050 1060 1070 1080 1090 1100 1110
TTCAGAGTTCAGAGTCCAGGCCCGCCAGCCCTCTCCTCCTCAGACCAGGAGTCCAGCCCTCTCCTCCTC
TTCAGAGTTCAGAGTCCAGGCCCGCCAGCCCTCTCCTCCTCAGACCAGGAGTCCAGCCCTCTCCTCCTC
1000 1010 1020 1030 1040 1050 1060
CTCAGAGTTCAGAGTCCAGGCCCGCCAGCCCTCTCCTCCTCAGACCAGGAGTCCAGCCCTCTCCTCCTC
CTCAGAGTTCAGAGTCCAGGCCCGCCAGCCCTCTCCTCCTCAGACCAGGAGTCCAGCCCTCTCCTCCTC

410 420 430 440 450 460 470 480

580 590 600 610 620 630 640

ACTCCTCAACGGTGACTCTGGGGGCCCTCATCTGCAACGGGTACTTGCAGGGCCCTTGCTCTTTTCGGA

ACTCCTCAACGGTGACTCTGGGGGGCCCTCATCTGCAACGGGTACTTGCAGGGCCCTTGCTCTTTTCGGA

490 500 510 520 530 540 550

AAGCCCCGTGTGGCCAGTGTGGCGTGCAGGTGCTTACACAACTCTGCAAAATTCACCTGAGTGGATAGAG

AAGCCCCGTGTGGCCAGTGTGGCGTGCAGGTGCTTACACAACTCTGCAAAATTCACCTGAGTGGATAGAG

560 570 580 590 600 610 620

AAGCCCGTGTGGCCAACTTGGCGTGCCAGGTGCTTACACAACTCTGCAAAATTCACCTGAGTGGATAGAG

630 640 650 660 670 680 690 700 710 720

AAACCGTCCAGCCAGTAACTCTGGGACTTGGAAACCCATGAAATTCACCCCAAAATACATCTCGGGAA

AAACCGTCCAGCCAGTAACTCTGGGACTTGGAAACCCATGAAATTCACCCCAAAATACATCTCGGGAA

730 740 750 760 770 780 790

GAATTCAGGAATATCTGTTCACGCCCTCTCTCCAGCCCTCTCCCTCAGCCCGAGAGTCCAGGCCCCAGCCCTCTCTCC

GAATTCAGGAATATCTGTTCACGCCCTCTCTCCAGCCCGAGAGTCCAGGCCCCAGCCCTCTCTCTCC

700 710 720 730 740 750 760

TCAAACCAAGGGTACAGATCCCGAGCCCTCTCTCCCTCAGCCCGAGAGTCCAGGCCCCAGCCCTCTCTCC

TCAAACCAAGGGTACAGATCCCGAGCCCTCTCTCCCTCAGCCCGAGAGTCCAGGCCCCAGCCCTCTCTCC

770 780 790 800 810 820 830 840 850 860

CTCAGACCCAGAGTCCAGCCCTCTCTCCCTCAGCCCGAGAGTCCAGGCCCCAGCCCTCTCTCTCC

CTCAGACCCAGAGTCCAGCCCTCTCTCCCTCAGCCCGAGAGTCCAGGCCCCAGCCCTCTCTCTCC

870 880 890 900 910 920 930

CNTCAGACCCAGAGTTCAGAGCCCTCTCTCCCTCAGCCCGAGAGTCCAGGCCCCAGCCCTCTCTCTCC

CNTCAGACCCAGAGTTCAGAGCCCTCTCTCCCTCAGCCCGAGAGTCCAGGCCCCAGCCCTCTCTCTCC

940 950 960 970 980 990 1000

GACCCAGGGGTTCAGGCCCTCTCTCCCTCAGCCCGAGAGTCCAGGCCCCAGCCCTCTCTCTCC

GACCCAGGGGTTCAGGCCCTCTCTCCCTCAGCCCGAGAGTCCAGGCCCCAGCCCTCTCTCTCC

1010 1020 1030 1040 1050 1060 1070 1080 1090 1100

GACCCAGGGGTTCAGGCCCTCTCTCCCTCAGCCCGAGAGTCCAGGCCCCAGCCCTCTCTCTCC

GACCCAGGGGTTCAGGCCCTCTCTCCCTCAGCCCGAGAGTCCAGGCCCCAGCCCTCTCTCTCC

1110 1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220

CAGACCCAGAGTTCAGGCCCTCTCTCCCTCAGCCCGAGAGTCCAGGCCCCAGCCCTCTCTCTCC

CAGACCCAGAGTTCAGGCCCTCTCTCCCTCAGCCCGAGAGTCCAGGCCCCAGCCCTCTCTCTCC

1230 1240 1250 1260 x

GNACAGTGCCTCCCTTGGTGGNAGTTGACCAACCTTACAGTGGTTTTTCATTTTNGTCCCTTCC

GNACAGTGCCTCCCTTGGTGGNAGTTGACCAACCTTACAGTGGTTTTTCATTTTNGTCCCTTCC

1270 1280 1290 1300 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400

GTACACAGTGCCTCCCTTGGCANGTTGACCAACCTTACAGTGGTTTTTCATTTTNGTCCCTTCC

GTACACAGTGCCTCCCTTGGCANGTTGACCAACCTTACAGTGGTTTTTCATTTTNGTCCCTTCC

1410 1420 1430 1440 1450 1460 1470 1480 1490 1500

TAGATCCAGAAATAAGTTTAAGAGGCGCAAAAAA

TAGATCCAGAAATAAGTTTAAGAGGCGCAAAAAA

1510 1520 1530 1540 1550 1560 1570 1580 1590 1600

TAGATCCAGAAATAAGTTTAAGAGGCGCAAAAAA

TAGATCCAGAAATAAGTTTAAGAGGCGCAAAAAA

4. US-09-030-606-173 (1-1265)
US-09-030-747-17 sequence 174. Application US/09020747

Initial score	=	529	Optimized Score	=	688	significance	=	7.74
Residue Identity	=	59%	Matches	=	710	Mismatches	=	454
Gaps	=	31	Conservative Substitutions	=			=	0

50 60 70 80 90 X 100 110
GGAAACGAATTGTTCTGCTCGGGCGTCTGGTGCATCCGCACTGGGTGCTGTCTAGCGGCACACTGTTTCCA

150	170	180	190	200	210	220
-----	-----	-----	-----	-----	-----	-----

170 180 190 200 210 220 230
GGCAGGGAGCCAGATGGTAGGCCAGCCTTCGTCAGCGCACCCAGAGTACACAGACACCTTCTCTCGCTAA
ACACAGACACCTTCTCTCGCTAA
X 10 20

[illegible]

390 400 410 420 430 440 450
TGCTGTGCGCCCTCTTCAAGAGGTCTCTGCCAGTCGCGGGGCTGACCCAGAGCTCTGCGTCCGAGGC
|||
GGC

AGAAATGCGCTACCGTGCAGTCGGTGGAACGTGTCGGTGGTCTGAGGAGGTCTGCAGTAGCTCTATGAC
AGAAATGCGCTACCGTGCAGTCGGTGGAACGTGTCGGTGGTCTGAGGAGGTCTGCAGTAGCTCTATGAC

	530	540	550	560	570	580
CCGCTGT	TACCA	CCCCAG	CTTCT	CGCGCG	GAGCA	CCAGAGGACTCC
CCGCTGT						
230	X					

7. US-09-030-606-173 (1-1265)
22 00-747-45 sequence 45. Application US/09020747

Initial Score	=	155	Optimized Score	=	204	Significance	=	1.88
Residue Identity	=	73%	Matches	=	234	Mismatches	=	0
Gaps	=	-	Conservative Substitutions	=	83		=	0

170 180 190 200 210 220 230
 GGCAGGAGGCAGATGGTGGAGCCAGCCTCGTAGCCACCAGAGTACAACAGACCTTGGTCGCTAA
 ACAACAGACCCCTTGGTCGCTAA
 y 10 20

CGACCTCATGCTCATCAAGTTGGAGATTCGGTTCGGAGCTTGACACCATCCGGAGCATCAGCATTGCTTC
|||||
CGACCTCATGCTCATCAAGTTGGAGATTCGGTTCGGAGCTTGACACCATCCGGAGCATCAGCATTGCTTC
|||||

GCAGTGCCTTACCGCGGGAACTCTTGCCTCTCTTTCGGCTGGGGTCTGTCGCCAACGGTGCAGCTCAACGGG
110 320 330 340 350 360 370 380
GCAGTGCCTTACCGCGGGAACTCTTGCCTCTCTTTCGGCTGGGGTCTGTCGCCAACGGTGCAGCTCAACGGG
120 320 330 340 350 360 370 380

100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450

TTGTCTCTGCCCTTCACGAGGCTCTGCCAGTCGCGGGGCTACCCAGAGCTCTGCTGCCACGC
111
-----GSC

460
470
480
490
500
510
520

AGAATGCCTACCGTGCTGCATCGTCGGTGGTCTCGAGGAGGTCTGCAGTAAGCTCTATGAC
AGAATGCCTACCGTGCTGCATCGTCGGTGGTCTCGAGGAGGTCTGCAGTAAGCTCTATGAC
AGAATGCCTACCGTGCTGCATCGTCGGTGGTCTCGAGGAGGTCTGCAGTAAGCTCTATGAC
AGAATGCCTACCGTGCTGCATCGTCGGTGGTCTCGAGGAGGTCTGCAGTAAGCTCTATGAC

8. US-09-030-606-173 (1-1265) Application US/08806596

8. US-09-030-606-173 (1-1265)
US-09-030-606-23 sequence 23. Application US/08806596

US-08-006-350-23	Sequence	Initial Score	Optimized Score	Significance
	Initial Score	93	240	0.91
	Residue Identity	30%	276	594
	Gaps	30	Conservative Substitutions	0

GCCTCGCAGTCCCTACCCGGGGACTCTTGCTCGCTCTTCTGGCTGGGCTGTCTGGCGAACGGTGAAGCTC
310 320 330 340 350 X 360 370
GGCGAAAGTACTACTCGCTCGN
X 10 20

380 390 400 410 420 430 440
 AACGGTGTGTCCTGCGCCCTTCAAGGAGGCTCTGCCAGTCGGGGGGTGACCCAGAGCTTCTCGGTCC
 ATCTTCTGGCGCTCGCTNCTCTT-----TTCTCCGGACCACTGCTGCNACNCCGATTTNGCGNATATCNAN
 90 70 80 90

450
CAGGACGAATGCCCTACCGTGCAGTCGGTGAACGTCTCGGTGGTCTTGAGGAGCTCTGCAGTAAGCTCT
||| || |
AAGNTCGANCACTCCAAACTGANTAACACACACACNCNANAGANAATCCNCTGCCTTCCANAGTAGTANACNAT
100 110 120 130 140 150 160

20 ATCACCGCTGTACCAACCCAGCATGTTTGGCCGGCGAGGGGCAAGACGACGAGCATCTCTCGAACCGGTG
 30 530 540 550 560 570 580 590
 TGAACNAGAGAACCAACGNCGCGGAATAGCGCTCGCGCC-----GCCAATNTGTTCNCGGTTTT
 40 190 200 210 220

ACTCTGGGGGCCCCGTATCGAACGGGTACTTGCAGGCCCTTGTCGTTCTCGAAAGACCCCGTGTGGCC
ATTWTCCAGCTCNCNCCNCCNACCCTAC TCTCTNNAGCTCTCNNAACCTCTCNNAACCTCTNCGNACCCCCCAGGT

670 680 690 700 710 720 730
 AAGTTGGCGTCCAGGTGTCTACACCAACTTCGCAATTCACCTGAGTGGATAGAGAAACCGTCCAGGCCA
 GGGATCGGGTTTTNNNTTACCGGNCNCCCTCCGCCCTCATNA -CGANCCNCCGCGACCAACCNNGC
 350 360

740 750 760 770 780 790 800
 GTTAACTCTGGGACTGGRACCCAGAAATTCACCCCAATATACATCTCGCGAAGGAATTCAGGAATATC
 NCGMCCCGCGNNCTTTCTGGCCNCCCTGCTCTNTNCCCTGCTGCNCGNCCGCAATGA-----
 420 430

TGTTCACGCGCCTCTCCCTCAGGCCAGAGTCCAGGCCCTCTCTCTCAAAACCAGGTTACT
870 860 850 840 830 820 810

880 AGATCCCGAGCCCTCTCTCTCAGACCCAGAGTCCAGACCCCTCTCTCTCAGACCCAGAGT
 900 910 920 930 940 950
 500 GCCTCTCTCCNNCNCCTTCCACGATCTCTTACNGGGTCTCCNCGCCTCTCNCNACNCCCTGGGACGG
 510 520 530 540 550 560 570

TCCAGCCCTCTCCNTCAGACCCAGGAGTCCAGACCCCGCCCTCCTCCCTCAGACCCAGGGTTGA

GTGGATAGAGAAACCGTCCAGGCCGATATTCATCGGAATCCTCGTCGAA
TTGCATGGCAGGACAGGCGAGGCCAGGCCAGGGTTGCTGTGATTATCCGAATANTCCTCGTCGAA

640 650 660 670 680 690 700
GTCTTTTCGAAAAAGCCCGGTGTGGCAAGTTGGCGTGCCAGTGTCTACACCAACCTCTGCAAAATTCACCTGA

710 720 730 740 750 760 770 780
GTGGATAGAGAAAACCGTCCAGCCAGTTACTTGGGGACTGGGACCCATGAATTGACCCCAATACA

TTCATGGCAGGGACAGGGGCCCCCAAGGCCCGCCCTT

CACT--TCGCCATCAGCGAGTATTAACAAAGGCCCAAGATGACTACTACAGACCTTCGCTCGGGTACT
 240 250 260 270 280 290 300

550 560 570 580 590 600 610
TCTGGCGCGGGAGGGCAACGACGAGAGACTCCTGCACGGTGACTCTGGGGGGCCCTGATCTGCAG

NTGAGTCGATTACGGCGGCTCACTGGCGGTCGTTTACAAACGCTCGTGAACCTGGGAAACCCCTGGCGGCTTACC
440 450 460 470 480 490 500

670 680 690 700 710 720 730
GCCAAGTTGGCGGTGCCAGGTGTTACACCAACTCTGCAAAATTCACCTGAGTGATAGAGAAAACCGTCCAGG
AACTTAATCGCCTTGCAGACATATCCCCCTTTCGCCAGCTGGGCGTAATANGAAAGGCCGCCACCGATCGC
510 520 530 540 550 560 570

740 750 760 770 780 790 800
CCAGTTAACTCTGGGACTGGGAACCCATGAATGACCCCAATATACATCCTCGGAAGAAATTCAGGAAT
ATCTGTCCAGCCCTCTCCCTCCTCAGCGCCAGAGTCCAGGCCCCAGCCCTCCCTCCCTCAAAACCAAGG
111 111 111 111 111 111 111
CCTTCCAACAGTTGGCACTGAATGGGNAATGGGACCCCCCTGT-TACGCGCATTTNAAACCCCGGNGG
590 600 610 620 630 640 650
TTTNGTGTATTACCCCACTNNACCGGTTACATTTTCCAGGCGCTTANCGCGCGTCCCTTTCCGCTTCT
660 670 680 690 700 710 720

810 820 830 840 850 860 870
TACAGATCCCCAGCCCTCTCCCTCAGAGCCAGAGTCCAGACCCCGCCGCTCTCTCCCTCAGACCCAG
TCCCTTCCTTTNCMCNCCTTTCCCGGGGTTCCCCNTCAACCCGNA
730 740 750 760 770 780 790
GAGTCCAGCCCTCTCCNTCAGACCCAG

950 960 970
GAGTCCAGCCCTCTCCNTCAGACCCAG

980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100 2110 2120 2130 2140 2150 2160 2170 2180 2190 2200 2210 2220 2230 2240 2250 2260 2270 2280 2290 2300 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400 2410 2420 2430 2440 2450 2460 2470 2480 2490 2500 2510 2520 2530 2540 2550 2560 2570 2580 2590 2600 2610 2620 2630 2640 2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760 2770 2780 2790 2800 2810 2820 2830 2840 2850 2860 2870 2880 2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990 3000 3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120 3130 3140 3150 3160 3170 3180 3190 3200 3210 3220 3230 3240 3250 3260 3270 3280 3290 3300 3310 3320 3330 3340 3350 3360 3370 3380 3390 3400 3410 3420 3430 3440 3450 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650 3660 3670 3680 3690 3700 3710 3720 3730 3740 3750 3760 3770 3780 3790 3800 3810 3820 3830 3840 3850 3860 3870 3880 3890 3900 3910 3920 3930 3940 3950 3960 3970 3980 3990 4000 4010 4020 4030 4040 4050 4060 4070 4080 4090 4100 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200 4210 4220 4230 4240 4250 4260 4270 4280 4290 4300 4310 4320 4330 4340 4350 4360 4370 4380 4390 4400 4410 4420 4430 4440 4450 4460 4470 4480 4490 4500 4510 4520 4530 4540 4550 4560 4570 4580 4590 4600 4610 4620 4630 4640 4650 4660 4670 4680 4690 4700 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 4910 4920 4930 4940 4950 4960 4970 4980 4990 5000 5010 5020 5030 5040 5050 5060 5070 5080 5090 5100 5110 5120 5130 5140 5150 5160 5170 5180 5190 5200 5210 5220 5230 5240 5250 5260 5270 5280 5290 5300 5310 5320 5330 5340 5350 5360 5370 5380 5390 5400 5410 5420 5430 5440 5450 5460 5470 5480 5490 5500 5510 5520 5530 5540 5550 5560 5570 5580 5590 5600 5610 5620 5630 5640 5650 5660 5670 5680 5690 5700 5710 5720 5730 5740 5750 5760 5770 5780 5790 5800 5810 5820 5830 5840 5850 5860 5870 5880 5890 5900 5910 5920 5930 5940 5950 5960 5970 5980 5990 6000 6010 6020 6030 6040 6050 6060 6070 6080 6090 6100 6110 6120 6130 6140 6150 6160 6170 6180 6190 6200 6210 6220 6230 6240 6250 6260 6270 6280 6290 6300 6310 6320 6330 6340 6350 6360 6370 6380 6390 6400 6410 6420 6430 6440 6450 6460 6470 6480 6490 6500 6510 6520 6530 6540 6550 6560 6570 6580 6590 6600 6610 6620 6630 6640 6650 6660 6670 6680 6690 6700 6710 6720 6730 6740 6750 6760 6770 6780 6790 6800 6810 6820 6830 6840 6850 6860 6870 6880 6890 6900 6910 6920 6930 6940 6950 6960 6970 6980 6990 7000 7010 7020 7030 7040 7050 7060 7070 7080 7090 7100 7110 7120 7130 7140 7150 7160 7170 7180 7190 7200 7210 7220 7230 7240 7250 7260 7270 7280 7290 7300 7310 7320 7330 7340 7350 7360 7370 7380 7390 7400 7410 7420 7430 7440 7450 7460 7470 7480 7490 7500 7510 7520 7530 7540 7550 7560 7570 7580 7590 7600 7610 7620 7630 7640 7650 7660 7670 7680 7690 7700 7710 7720 7730 7740 7750 7760 7770 7780 7790 7800 7810 7820 7830 7840

[illegible]

530 540 550 560 570 580 590
 CTGTACCAACCCGACATGTTCTCGCGCGCGAGGCGAAGACCAAGAGACCTCCGACCGTGACTCTCGG

CCCTTCAAGAGGTCTCTCCCAAGTCGGGGGGTGACCCAGACTCTGGTCCAGGCAGAAATGCCT


```
|||||
CCCAGCGTCACTTCTGCTGGANAATATTCTTTGCTCTTTTGGACATCAGGCTTGATGTTATCAGTCCCA
310 320 330 340 350 360 370 380
CGGTCTCGAGTGGTG-----AACGTGTCGGTGGTCTGAGAGGCTCTGAGTCTAGCTCTATGACCGG
|||||
CMTTCCACCCAGCTGGCCNCCCTTCCGCCATNTTGTCAANTGANCTGGAAGGCTGAANCTTAGTCTCCAA
390 400 410 420 430 440 450
530 540 550 560 570 580 590
CTGTACACCCAGCATGTTCTGCGCGCGGAGGAGGACCAAGACGACTCTCTGCAACGCTGACTCTGGG
|||||
AAGTCTCNGCCCAAGACCGCGCCACCAAGGGANGTCTNTTNCAGTGGATCTGC-----CAAA
460 470 480 490 500 510
600 610 620 630 640 650 660 670
GGGCCCCGTGATCTGCAACGGGTACTTGCAGGGCCTTGTCTTTCCGAAAGCCCGCTGTGGCCAAAGTGGC
|||||
ANTACCCNTATCATCCTNNTGAATAAAAGGCCCTGGAACGANATGCTTCCANCAACCTTTAAGACCCATAATC
520 530 540 550 560 570 580
680 690 700 710 720 730 740
GTGCCAGTGTCTACACCACTCTGCAAAATCACTGAGTGATGATGAGAAACCGTCCAGGCCAGTTAACTC
|||||
CTNGAACCATGGTGCCTTCCGGTCTGTATCCNAAAGGAATGTCTCGGTGCCANTCCCTCTCTTTGTTNCTT
590 600 610 620 630 640 650
750 760 770 780 790 800 810
TGGGACTTGGGAACCCATGAATGACCCCAATATACATCTCGGGAAGG-----ATTGAGGAATATCTGT
|||||
ACGTTGTTNTGGACCCNTGCTNGNATNACCAANTGANATCCCCNAGACACCTTNCCTCTGGCAATTTGANT
660 670 680 690 700 710 720
820 830 840 850 860 870 880
TCCAGCCCTCTCTCCCTCAGAGCCAGGAGTCCAGGCCCGCCAGCCCTCTCTCTCAACCAAGGTACAGA
|||||
TTCNTAAATCTCTGCCCTCACTNCTGAAAGACACNATTCCTCTGNGCNCNNAAGNGAACTCAAGAAGTCTN
730 740 750 760 770 780 790 800
890 900 910 920 930 940
TCCCGAGCCCTCTCTCTCAGACCCAGGAGTCCAGACCCCGCCAGCCCTCTCTCTCTCAGACC
|||||
NGMAAACCAACN
810 X
```

27. US-09-030-606-173 (1-1265)
US-09-020-747-16 Sequence 160, Application US/09020747

Initial Score = 59 Optimized Score = 126 Significance = 0.38
Residue Identity = 38% Matches = 148 Mismatches = 219
Gaps = 15 Conservative Substitutions = 0

```
X 10 20 30 40 50 60 70
GGCAGCCGCACTCCAGCCCTCTGGAGCGGCACTGTGTCATGGAAAGAAATGTTCTGTCGGCGCTCGTG
|||||
ACCTGCATCCAGCTTCTCCCTGCCAAACTCACAAAGAGAGACATCAACCTCTAGACAGGAAACAGCTTCAGG
X 10 20 30 40 50 60
80 90 100 110 120 130
GTGCATTC- GAGTGGGTGCTGTCAGCCGCA-----CACTGTTTCCAGACCTCTTACACATCTGGGCTGGCC
|||||
ATACTTCCAGGAGACAGAGCCACCAAGCAACAAATATTTCCCATCTGGAGCATGGCATAGAGGAAGC
70 80 90 100 110 120 130 140
140 150 160 170 180 190 200
TGCACAGCTTTGAGCCGACCAAGACGAGGAGCCAGCATGTGGA-----GGCCAGGCTCTCCGTAGC
|||||
TGANAATGTGGGTCTGAGGAAGCAATTTGAGTCTGGCCACTAGACATCTCATCAGGCACTTGTGTGAAGA
150 160 170 180 190 200 210
210 220 230 240 250 260 270
```

```
GCACCCAGAGTACACAGACGCCCTTCTCGCTAACGACCTCATGCTCATCAAGATTGGACGAATCCCTGTGCCGA
|||||
GATGCCCATGACCCAGATGCTCTCCACCCCTTACCTCCATCTCACACACTTTCAGCTTTCACACTCTGTAT
220 230 240 250 260 270 280
280 290 300 310 320 330 340
GTCTGACACCATCCCGGACATCAGCATTTCTTCGAGTGCCTACCGGGGAACTCTTTGCCCTCTCTTCTGG
|||||
AATTCTAATCTCTCTGGAGAAATGGCAGTTTTCAGCGAACCCTGTTTCAACAG- -GTAGAGGCTGATTTCTAA
290 300 310 320 330 340 350
350 360 370 X 380 390 400 410
CTGGGCTGTCTGGCGAACGAGTGTAGCTCACGGGTGTGTCTTCCCTCTTCAAGGAGTCTCTCTGCCAGTCT
CGAAACTTGTAGATGAAGCCTTGA
360 370 380
420
GCG
```

28. US-09-030-606-173 (1-1265)
US-08-904-809-40 Sequence 40, Application US/08904809

Initial Score = 59 Optimized Score = 249 Significance = 0.38
Residue Identity = 36% Matches = 279 Mismatches = 462
Gaps = 30 Conservative Substitutions = 0

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GAGCATCAGCATTTGCTCGCAGTGCCTTACCGCGGGAACCTCTTCCCTGCTTCTGCTGGGGTCTCTGTGGC
300 310 320 330 340 350 360
GAGCATCAGCATTTGCTCGCAGTGCCTTACCGCGGGAACCTCTTCCCTGCTTCTGCTGGGGTCTCTGTGGC
370 380 390 400 410 420 430
GAAAGCTGAGCTCAGCGGTGTGTCTGCTCCCTCTTCAAGGAGGTCTCTGCCCCAGTCTGGCGGGGTGACCCA
|||||
GTGTTCTCTCCCTCTGAGTGTAGAGGAAACACCTCTCATAGATGAACACCCCGCCCGAGACGACGACGTCGAA
30 40 50 60 70 80 90
440 450 460 470 480 490 500
GAGCTCTGGTCCCAAGCAGATGCTTACCGTGTGTCAGTGGTGAAGCTGCTGCTGTCTGAGGAGGTC
|||||
CTGCCAAGCAGCGGGTAGAGGGCGCCTTATGCACAGCTGGGGCCTTGAGACAGCAGCTCTCGATGTC
100 110 120 130 140 150 160
510 520 530 540 550 560 570
TGCAGTAAGCTCTATGACCCGCTGTACCAACCCAGCATGTTCTGCGCGGCGGAGGCAAGACAGAGGAC
|||||
AGGCTCGATGTCAATGGTCTG-----GAAGCGGGCGCTGTACCTGCGTAGGCGCACACCTCAGG--
170 180 190 200 210 220
580 590 600 610 620 630 640 650
TCCTGCAACGCTGACTTGGGGGGCCCTGTATCTCAACGGGTACTTGCAGGGCTCTGTGCTTTCGGGAAA
|||||
GCCACCAAGAACTTCTCAAAGTCTCCAGCAACNTGTTGCGACACACCGGAGACGAGTGTATNAGCTTGGG
230 240 250 260 270 280 290
660 670 680 690 700 710 720
GCCCGCTGTGGCCAAGTTGGCGTCCAGGTGTCTACACCACTCTGCAAAATCTACTGAGTGGATAGAGAA
|||||
GTTCGTCTAANCGCGGTGGCGTCTGCTGGAGCTGGCAGGGCTCCCGCAGGAAGCNAATAAAGGTG
300 310 320 330 340 350 360 370
730 740 750 760 770 780
ACCGTCCAGGCACTTACTCTGGGAGTGGGAACCCATGAATTTGACCCCAA-----ATACAT
|||||
CGCCCCCGACCGTTCANCTGCACTTCTCNAANACCATGANGTTGGGCTCNAACCCACCAACNCCGAC
380 390 400 410 420 430 440
790 800 810 820 830 840 850
CCTGCGGAGGAATTCAGAAATATCTGTCTCCAGCCCTCTCTCTCCAGGCGGAGGATCCAGGCCCCCAGC
|||||
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[illegible]

GATTTC

29. US-09-030-606-173 (1-1265)
US-08-806-596-26 Sequence 26, Application US/08806596

Initial Score	=	59	Optimized Score	=	197	Significance	=	0.38
Residue Identity	=	30%	Matches	=	204	Mismatches	=	461
Conservative Substitutions	=	2					=	0

550 560 570 580 590 600 610 620
GCGCGCGGAGGGCAAGACCAAGGACTCCTGCAACGGTGACTCTGGGGGGCCCTGATCTGCAACGGT

ANATTANTACAGTGTAACTTT
X 10 . 20

ACTTGCAGGGCCTTGTGTCTTTTCGAAAAGCCCGTGTGGCCAAAGTTGGCGTGCCAGGTGTCTACACCAACC

TCCCAGAGTGTGTANAGGGAACGGGGCCCTAGAGGCCATCCCANAGATATCTATATCAGAGAGCTCTTGGC

-TCTGCAATTCACTGAGTGGATAGAGAAAACCGTCCAGGCCAGTTAACTCTGGGACTGGGAACCCATGAA

Sequence	100	110	120	130	140	150	160
AAAGACCTGCTGGGACGATTCCTGAGGAGGATG							

ATTGACCCCCCAATACATCCTGGGAAGGAATCAGGAATATCTGTTCCCAAGCCCTCCTTCCCTCAGGGCCCC

	170	180	190	200	210	220	230
170							
180							
190							
200							
210							
220							
230							

C

GAGTCCAGGGCGGCCAGCCCCCTCCTTCCTCAACCAAAGGGAACAATCCCAGCCCCCTGCCTTTGTGTA
— — — — —
T

ATTTCATCATCACCATGGCGCGGGAGGAGGAGCGCTCTTGCTGNACCGGGGTGGCANANAGCCTANTCAGAGGGGT
—————

240	250	270	280	290	300
910	920	930	940	950	960
970	980	990	1000	1010	1020

AGGAGTCCACAGACCCCCCCCCTGGCCTGCCTGCTTCAGGTGCACCCCTTCTTACCCTGACNACCAGNAC
CACACTATAAACGTTTAACGCCACCNAGATNANCACTGCTTCAAGTGCACCCCTTCTTACCCTGACNACCAGNAC

30. US-09-030-606-173 (1-1265)
US-08-904-809-66 Sequence 66, Application US/08904809

Initial Score	=	58	Optimized Score	=	115	Significance	=	0.30
Residue Identity	=	41%	Matches	=	131	Mismatches	=	174
Gaps	=	10	Conservative Substitutions	=	0		=	0

GTCCAGGCCCCAGCCCTCTCCCTCAACCCAGGTACAGATCCCGAGCCCTCTCCCTCAGACCCGAG
0 850 860 870 880 890 900 910
ACGCCCTTCCCTCAGAAATTCAG
X 10 20

AGTTCAGAGCCCGCCCTCCTCCCTCAGAGGATTCAGAGCCCTCCTCCTTCAGAGCCAGGATCC
GGAAGAGATGTCGGCTCCTCCCTCCTGTTGGGTGAGAACCGGTGCC---CCTTCCGCCCATC
920 930 940 950 960 970 980

AGACCCCGCAGCCCTCTCTCCCTCAGACCCAGGGTTGAGCCCCCAACCCCTCTCTTCAGAGTCAGAGG

1060 1070 1080 1090 1100 1110 1120
TCCAAGCCCCCACCCTCGTTCCCCAGACCAGAGGTTNAGGTCCCGAGCCCTCTTCCTCAGACCCAGNG

TTACCCCTGATCCCCCAGCATCCCGAATTC
60 170 180 190 200 210 220

11130 1140 1150 1160 1170 1180 1190
GTCCAATGCCACTAGATTTCCTGNACACAGTGCCTTGNGANGTTGACCAACCTTACCAGTTGG

TTTATGGGTTTATATATATTTTAAAGATGCACCTTTATGTGCTATTTTAAAGAGTCTGAAGAAATTA
230 240 250 260 270 280 290 300

1 1 1 1
TGTTT x
x

[illegible]

35. US-09-030-606-173 (1-1265) Application US/09020747

Initial Score	=	57	Optimized Score	=	429	Significance	=	0.34
Residue Identity	=	36%	Matches	=	466	Mismatches	=	783
Gaps	=		Conservative Substitutions	=	44		=	0

10 20 30 40 50 60 70
 GCGAGCCGCACTCGCAGCCCTGGCAGCGGCATGTGTATGGAACGAATGTTCTGCTCGGCGCTCTG
 AGCCAGGGTCCCTCTGCTGCTGCCACTGCTGGCAACACCCGGAGCTGTTTGTCTC--CTTT
 X 10 20 30 40 50 60
 80 90 100 110 120 130
 GTGCATCCGCACTGGGTGTGTGACGGCGACACTGTTTCAGAACTCCTA----CACCATCGGCTGGGCGC
 TGGAGCCTCAGCAGTTTCCCTCTTTTCAGAACTCACTGCCAAGAGCCCTGACAGGAGCCACCATGCAGTGGCT

[illegible]

34. US-09-030-606-173 (1-1265) Application US/09020747

Initial Score	=	57	Optimized Score	=	250	Significance	=	0.34
Residue Identity	=	38%	Matches	=	289	Mismatches	=	442
Gaps	=	29	Conservative Substitutions	=			=	0

X 10 20 30 40 50 60 70
 TGGCAGCCGCACTCGCAGCCCTGGCAGCGGCACTGGTCATGGAACCAATTTCTGCTCGCGGCTCCTG
 GTGAGAGCCAGCGTCCCTCTGCTGCCCACTCAG---TGCACACCCCGGAGACTGTTTTTCTTCTTTGTG
 X 80 90 100 110 120 130 140
 TTGTCATCCGCAAGTGGTGTCTCAGCCGCACATGTTTCCAGAACT---CCTACACCATCGGCTGGCGCTG
 TGGAGAGCCTCAGCAGTCCCTCTTTTCAG-ACTCACTGCCACAGCGCCTGAACAGGAGCCACCATGCAGTGTCTC
 150 160 170 180 190 200 210
 CACAGCTCTTGAAGCGCGACCAAGAGCGCAGGAGCCAGATGTTGGAGGCCAGCCTCTCCGTACGGCACCCAGAG

[illegible]

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38.  US-09-030-606-173 (1-1265)
      US-09-020-747-13 Sequence 13, Application US/09020747

      Initial Score      = 56      Optimized Score = 251      Significance = 0.33
      Residue Identity   = 38%      Matches        = 281      Mismatches  = 439
      Gaps                = -        Conservative Substitutions = 0

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120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000

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37. US-09-030-606-173 (1-1265)
   US-08-904-809-13 Sequence 13, Application US/08904809

Initial Score = 56 Optimized Score = 251 Significance = 0.33
Residue Identity = 38% Matches = 281 Mismatches = 439
Gaps = 16 Conservative Substitutions = 0

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[illegible]

[illegible]

550 560 570 580 590 600 610
ATGTTCTGCGCC--GGCGGAGGCAAGACAGAGGACTCTCTCAACGGTGACTCTGGGGGGCCCGCTGATCT

100 110 120 130 140 150 160
NACTACGCCCNCAACNACGACGCTCTANNANATNCACCTGANNCGCGGANGTNGANNAGAAANCTATACCC

170 180 190 200 210 220 230
ANAGNCACANACNCCAGCTGTCCNANAAGCCTNNNATACNGNGNNATCCAAATNGNACNCTCNAAGTAT

240 250 260 270 280 290 300 310 320
TNNNCNANATGATTTCTTANCCGATACCCCTNCCGCTTANCCCTTCCCGCCCAACNACGAAGGNCCT--

330 340 350 360 370 380
GGNCCNAAAGNGCGNCCCGCTAGTTCCTCCCNCAAGTCNCNCCTTAACTCANCNNATATACNCGCT

390 400 410 420 430 440 450
CNTGAG---TATCACTCCCGAATCTCAACCTACTCAACTCAAAANAATCNGATACAAATAATNCAAGCT

460 470 480 490 500 510 520
GNTTATACAC-TNTGACTGGTCTTATTTAGNGGTCNTNANCNTCTTAATCTTCCAGTCTNCCTTC

530 540 550 560 570 580 590
-----NCCAAATTCNAAAGCTCTTCNCAAG----CATNTTTTGTGTCCCNNTTGGTTCCTTAN

600 610 620 630 640 650
NGAATGGCCTTCNTNGAAGGGCTCTTTCTTCGGTTANCCTGGNTTNNCCGGCAGTATATATT

660 670 680 690 700 710
CCCTTTTAAATTCNTNCCNTTANTTTTGGCNTC-----NAAACCCCGCGCTTGAAGAACGCGCCCTC

720 730 740 750 X
TGGTAAAGTGTGTTTTGANAATAATTTTGTTTGTCTC

760 770 780 790 800 810 820
GAACCATGAATTTGACCCCAATACATCTCGGGAAGGAATTCAGGAATATCTGTCCACGCCCTCTCTC

830 840 850 860 870 880 890
CCTCAGGCCCAGAGGTCCAGAGCCCCCAGGCCCTCTCTCCCTCAACCAAGGTACAGATCCCGACGCCCTCTC

900 910 920 930 940 950 960
CCCTCAGACCCAGAGGTCCAGACCCCCCAGGCCCTCTCTCAGACCCAGGATCCAGCCCTCTCTCCNTTC

970 980 990 1000 1010 1020 1030 1040
AGACCCAGAGTCCAGACCCCCCAGGCCCTCTCTCAGACCCAGGGGTGAGGCCCCCAACCCCTCTCTC

1050 1060 1070 1080 1090 1100 1110
TTCAAGTTCAGAGTTCAGAGCCCCCAACCCCTCTCTCCCGACACCCAGGTGNNAGTCCCGACCCCTCTCTC

1120 1130 1140 1150 1160 1170 1180
CNTCAGACCCAGNGTCCAAATGCCACTAGATTTCCCTGNACACAGTGCCTCTGTGGNAGTTGACCCCA

1190 1200 1210 1220 X 1230 1240 1250
ACCTTACCGATGGTTTTTCATTTTNGTCCCTTTCCCTCTAGATCCAGAAATAAGTTTAAAGANGNCA

1260
AAAAAAA

41. US-09-030-606-173 (1-1265) 26 Application US/09020747

US-09-020-747-26 Sequence 20, Approximate 50%			
Initial Score	=	36	Optimized Score = 239
Residue Identity	=	52%	Matches = 271
Gaps	=	19	Conservative Substitutions = 540
			Mismatches = 511
			Significance = 0.33

CTGCCCTCTCAAGAGGTCCTCTGCCAGTCGGGGGGTGACCCAGAGCTTCGCTCCAGGCAGATGC

[illegible]

GCCTCCAGTCCAGTCCACAC
X

290 300 310 320 330 340 350
CATCCGAGCATCAGCAATTCCTTCGAGTGCCTTACCGGGGAACTCTTCCTCGTTTCTGGCTGGGGTCT
CACCCAGGTGCTGCTAGTTTCGA-TGTATACAAGAGTGTATGAACACACCTCTACTCTTTTGGTCG
30 40 50 60 70 80 90

360 370 380 390 400 410 420
GCTGGCAACGGTGAAGTCTACGGGTGTGTCTGCGCTCTTCAAGGAGGTCTCTTGCCTGAGTTCGGGGGT
TGAGCTTTTGGCTTGGTGGAGTTTCATTCGGCTGTCTGGT-GAGTGTCTATTCGAACACAAGTGGGGAAA
100 110 120 130 140 150 160

430 440 450 460 470 480 490
GACCCAGAGTCTCGCTCCACAGGAGAATGCCTACCGTGC-TGCAGTGGCTGAA-CGTGTCGGTGGTGTCT
GGCACTGTCTCTTTGAAGTANGGTGAGTCTCTCAAAATCGTATAGTTGGTGAAGCACAGCACATGAGCCC
170 180 190 200 210 220 230

500 510 520 530 540 550 560
GAGGAGGTCTCGATAGCTCTATGACCCGCTGTACACCCGCTGTACACCCGAGCATGTTCTGCGCGCGGAGGGGCAAGAC
TTTCATGTTGTTTCCACATCTCAGTAGTCTTCTTGGGACCATATCTTCTTGTGATGCGACGACACTAC
240 250 260 270 280 290 300

310 320 330 340 350 360 370
CAGCAACGTCAGGAGTGTCTCAGCCATTGTGG-TGTACACCAAGCGCACACGAGCTGCNACCTCAGC
380 390 400 410 420 430 440
AATGAGATGANGAGGANGATCAAGAAGACCTCNCGAGGCGACATGCTCTCAGCTTANCACCATANCA
450 460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGCAGTGGGACAGTGGCCCNAAATCTTCAAAAAGTATGCCCCATCNATTTGACCCCCCAAA
-TGATGGCACTGGGACAGTGGCCCNAAATCTTCAAAAAGTATGCCCCATCNATTTGACCCCCCAAA
590 600 610 620 630 640 650

660 670 680 690 700 710 720
CTTATNATNACNTGAACCTCGTNTGTGGCTCTGT---TCAGGNCNNGGCTTGAATCTTNAANNAAGAAC
730 740 750 760 770 780 790

800 810 820 830 840 850
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGTCCGA--TGAAGAAATNACCCNCGTTCAGCAAACT
460 470 480 490 500 510 520

530 540 550 560 570 580 590
GCGAAGAAATTCAGGAATATCTGTTCACGAGCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
ATAGAGAAACCTCCAGGCGAGTTAATCTCTGGGACCTGGGAACCCATGAATTCAGCCCAATATCATCTCT
GCCTNTGAAACCAANANCAAGACCCACNACNCCGGT

55

30	40	50	60	70	80	
610	620	630	640	650	660	670
GGCCCCGATCTGCAACGGGTACTTGCAGGGCTTGTCCTTCGGAAGCCCGCTGTGGCCAAAGTTGGCG						
AAATNNCCATTTCCGGGGGGGTTCCAAACCCAAATTAATTTTGG-----NNTTAAATTAATATTTAT						
90	100	110	120	130	140	150
680	690	700	710	720	730	740
TGCCAGGTGCTACACCACTCTGCAAAATCTACTGAGTGGATGAGAGAAACCGTCCAGGCCAGTTAACTCT						
160	170	180	190	200	210	220
TNGGGGAANAANCCAAATGTNAGAAATTTAACCCATATNACCTTAAATNCCCTNGAAACCCNTGGNTTCC						
230	240	250	260	270	280	290
AAAATTTTAAACC--TTAATCTCCTCGAAATGTNTAAANGGAAACCAAAATTCNCCTAAGCTNTTTGAAG						
820	830	840	850	860	870	880
CCCTCCTCCTCCCTCAGGCCAGAGTCCAGGCCCCAGCCCTCTCCTCAACCAAGGATACAGATCCCCA						
300	310	320	330	340	350	360
GTTNGATTTAAACCCCTTNAATTTTTTTACCCNNGNCTNAANTATTTNGTTCGGTGT-----TTTCT						
370	380	390	400	410	420	430
NTTAANCNTNGTAACTCCCGNTAATGAANNCCCTAANCCAAATAAACCGCAATTTTTTTTGAATTTGGAAT						
960	970	980	990	1000	1010	1020
TCCTCCNTCAGACCAGAGTCCAGACCCCGCCAGCCCTCTCCTCAGCCAGGGGTTGAGCCCCCAAC						
440	450	460	470	480	490	500
TCCNNGGAATTNACCGGGTTTTTCCCTTTGGGGGCCATNCCCCCTTCGCGGGTTTGGG-----NNTA						
1040	1050	1060	1070	1080	1090	1100
CCCTCCTCCTTTCAGAGTCAGAGTCCAGGCCCAAGCCCAAGCCCTCGTTCCTCAGCCAGAGTNNAGTCCAC						
510	520	530	540	550	560	570
GGTTCGAATTTTTNANGNCCCAAAAAANCCCCCAANAAAAAACTCCCAAGNNTTAATTNGAATNTCCCTCT						
1110	1120	1130	1140	1150	1160	1170
CCCTCTTTCNTCAGACCCAGNGTCCAAATGCCACCTAGATTTTCCCTGNACAGTCCGCCCTTGTGGNAN						
1180	1190	1200	1210	1220	1230	1240
GTTGACCAACCTTACCAGTTGGTTTTTATTTTTNGTCCCTTCCCTTAGATCCAGAAATAAGTTTAAAG						
650	660	670	680	690	700	710
GGTAA-----ANGGTATNGNNTTTGGTTTTTGGGCCCTTNGAGACCTTCGGATNGAAAAATAAATTC						
1250	1260					
GANGNGCAAAAAA						
CCCGGNGCGCG						
720	x					

49. US-09-030-606-173 (1-1265)
US-08-904-809-12 Sequence 12, Application US/08904809

Initial Score	=	52	Optimized Score	=	245	Significance	=	0.27
Residue Identity	=	37%	Matches	=	290	Mismatches	=	458
Gaps	=	18	Conservative Substitutions	=			=	0

220	230	240	250	260	x	270	280
GTACAACAGACCCCTTGCTCCCTAACGACCTCATGCTCAAGTTGGAGCAATCCGTGTCCGAGTCTGACAC							

49. US-09-030-606-173 (1-1265) Application US/08904809

Initial Score	=	52	Optimized Score	=	245	Significance	=	0.2
Residue Identity	=	37%	Matches	=	290	Mismatches	=	458
Gaps	=	18	Conservative Substitutions	=			=	0

18 Conserved nucleotide sequence


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1060      1070      1080      1090      1100      1110      1120      1130
AAGCCCCCACACCCTCGTTTCCCCCAGAGGTNNAGGTCGCCAGCCCTCTTCCNTTGACACCAGNGTGC
|||||              |||||              |||||              |||||
NTCNGGCCANTNNGCTCAANCNCNACNAACCGCGCTGGCGGCCGNAGCGNCNCCTCCNCGACTCCTCT
730       740       750       760       770       780       790

        1140      1150      1160      1170      1180      1190
C---AATGCCACCTAGATTTCCTCTGNACACAGTGCCTCTGTGGNANGTTGACCCAAGCTTACCAGTTGG
|||||              |||||              |||||              |||||
CCGNCITCCNACCACGANNITCCNCGAGGACACNNAACCCGCGCNACGGGG
800       810       820       830       840       X

1200      1210      1220      1230
TTTTTCATTTTNGTCCTTTCCCTTAGATC

51. US-09-030-606-173 (1-1265)
US-09-020-747-38 Sequence 38, Application US/09020747

Initial Score = 51 Optimized Score = 208 Significance = 0.25
Residue Identity = 32% Matches = 245 Mismatches = 479
Gaps          = 31 Conservative Substitutions = 0

450   470   480   490   500   510   520
TG CCT ACC GGT C T G C A G T G C G T G A A C G T G C G T G T C T G A G G A G G T C T G C A G T A A G C T C T A T G A C C C G C
|||||              |||||              |||||              |||||
530   540   550   560   570   580   590   600
T G T A C C A C C C A G C A T G T T C T G C G C G G G A G G C A A G A C C A G A A G A C T C C T G C A A C G G T G A C T C T G G G G
|||||              |||||              |||||              |||||
TTTTTTTTTTTTAAAAAACCCCTCCCATGAATGAAATACTTCNAAAATGTGCCAACCCCTCNMC-----C
30    40    50    60    70    80

610   620   630   640   650   660   670
G G C C C T G A T C T C A A C G G G T A C T T G C A G G C C T T G T G T C T T G G A A A A C C C C G T G T G C C A A G T T A A C T C T
|||||              |||||              |||||              |||||
A A A T N N C C A T T T C C G G G G G G T T C C A A A C C C A A A T T A A T T T T G G A -----N T T T A A A T T A A A T N T N A T
90   100   110   120   130   140   150

        680   690   700   710   720   730   740
T G C C A G S T G T C T A C C A C C A C C T C T G C A A A T T C A C T G A G T G G A T A G A G A A A C C C T C C A G G C C A G T T A A C T C T
|||||              |||||              |||||              |||||
T N G G G A A N A N C C A A T G T N A G A A A A T T T A A C C C A T T A T N A C T T A A A T N C T I N G A A A C C C N T G G N T T C C
160   170   180   190   200   210   220

        750   760   770   780   790   800   810
G G G A C T G G G A A C C C A T G A A A T T G A C C C C A A A T A C A T C C T G C G A A G A G A T T C A G G A A T A T C G T T C C C A G
|||||              |||||              |||||              |||||
A A A A A T T T T A A C C - T T A A T C C C T C G A A A T T G N T A A N G A A A A C C A A A T T C N C C T A G G C T N T T T G A A G
230   240   250   260   270   280   290

        820   830   840   850   860   870   880
C C C C T C C C C T C A G G C C C A G A G T C C A G G C C C C C C A G C C C C T C C T C C C T C A A A C C A A G G G T A C A G A T C C C C A
|||||              |||||              |||||              |||||
G T T N G A T T T A A C C C C T T N A N T T T T T N A C C N G N C T N A A T A T T N G N T T C C G G T G T ----T T T C C T
300   310   320   330   340   350   360

        890   900   910   920   930   940   950   960
G C C C C T C C C C T C A G A C C C A G A G T C C A G A C C C C C C A G C C C C T C C T C C C T C A G A C C C A G G T T C C A G C C C
|||||              |||||              |||||              |||||
N T T A A N C N T N G T A A C T C C G N T A A T G A A N N C C C T A A N C C A A T T A A A C C G A A T T T T T T T T T T T T G A A T T G A A A T
370   380   390   400   410   420   430

        970   980   990   1000   1010   1020   1030
T C C T C N T C A G A C C C A G A G G T C C A G A C C C C C C A G C C C C T C C T C C C T C A G A C C C A G G G T T G A G C C C C A A C
|||||              |||||              |||||              |||||
T C C N G G A A T T N A C G G G T T T T C C N T T T G G G G C C A T N C C C C N C T T C G G G T T T G G G ---N W T A
440   450   460   470   480   490   500

1040     1050     1060     1070     1080     1090     1100
C C C T C C T T C A G A G T C A G A G T C A A G C C C C A A C C C C T C G T T C C C C A G A C C A G A G T N N A G G T C C C A G

```


GGTGAATTTTNNANGNCCCAAAAANCCCCCAAAAAAATCCCAAGNNTTAATTNGAATWTCCTT

1110
1111
CCCCCTTCCTCCAGACCGAGNGGTCCTAATGCCACCTAGATTTTCCCCTGNACACAGTGCCCCCTTGTGGNAN

580 550 520 490 460 430 400 370 340 310 280 250 220 190 160 130 100 70 40 10

1180 1190 1200 1210 1220 1230 1240

GTTCACCAACCTTACCAAGTGGTTTCATTTCCTTCCCCATAGATCCAGAAATAAAGTTTAAAGA

250 1260
GANGNGCAAAAAAAAAA

CCCGGGGCGGCCG 720 X

Initial Score	=	51	Optimized Score	=	253	Significance	=	0.25
Residue Identity	=	35%	Matches	=	305	Mismatches	=	494
			Conservative Substitutions	=	56			0

280 GACACCATCCGAGACATCAGCATTCCTCGAGTCCCTACCGGGGGAACCTTGCCTCTGTTTCTGCCTGGTGGT
 310 320 330 340
 CATTTCCGGGTTTACTTTCTAA
 y 10 20

GGTGTGTGGCGAAGCGTGAAGTCACGGGTGTGTCTTGCAGGAGGTCTCTTGCCACAGTTCGGCG

GGGTGACCCAGAGACTCTGGGTCCGAGGAGAAATGCCTACCTGCTGCTGAGTGGCTGAGACCTGTCGGGTGGTGTG

CTGAGGAGGTCGAGTAAGCTCTATGACCGCGTGTACACCCAGCATGTTCTGCGCGCGGAGGGCAA

[illegible]

640 220 230 240 250 260 270 280 700 710

C-----GCCACCCCTGACCTGCTGGGTCCAAACACTGAGCCCTGC-----TGGCGGAG
 290 300 310 320 330 340 350 360 370 380 390 400

340 TCAAGGANAACCCACACANGGGATTTTGGCTCTTANATAAGGCTCATCTGGGCTCGCCCCCCCCACCT 41
345
350
355
360
365
370
375
380
385
390
395
400
405
410

570 580 590 600 610 620 630
ACCAAGAGACTCTCTGCAAGGTTACTCTGTGGGGGCCCTGATCTGCAAGGGTACTTTCAGGGCT----T
AACTCAAGGGGAGTGGAAACCGTAAGCCCAATCTTANCAAGTGTGGGGGAAGACTGGTGCAGTCTCAAGC
30 40 50 60 70 80 90

640 650 660 670 680 690 700
GTGCTCTTCGGAAGAGCCCGCTGTGGCCAAAGTTGGCGTGCCAGGTGCTACACCAACCTCTGCAAAATTCAC
GAGTGGATAGAGAAACCGTCCAGGCCAGTTACTCTGGGAGCTGGGAACCCATGAATGACCCCCCAATA
110 120 130 140 150 160 170
GTGACATCTACTGGAGATCGGGGCCCAATGAGGACTCCTACGCAAGGCAAGCTGACCAACAGCAGACTAATTTCTGGCCC
180 190 200 210 220 230 240
GCCAGCTCAAAATGCTACTACTTGTATTACAANGAGCAGTCCCGGAGTACGCTATATGACACAGCTCTTG
250 260 270 280 290 300 310
CATCTCGGAAGAAATTCAGGAATATCTGTTCACGCCCTCTCCCTCAGGGCCAGGATCCAGGCCCCC
860 870 880 890 900 910 920
AGCCCTCTCCCTCAAAACAAGGATACAGATCCCGACCCCTCTCCCTCA--GACCACGAGGTCCAGACC
930 940 950 960 970 980 990
CCCCAGCCCTCCCTCCCTCAGACCCAGGAGTCCAGCCCTCTCCCTCAGACCCAGGATCCAGGCCCCCA
1000 1010 1020 1030 1040 1050 1060
GCCCTCTCCCTCAGACCCAGGAGTGGCGCCCAACCCCTCTCTCTCAGATCAGAGTCCCAAGCCCC
1070 1080 1090 1100 1110 1120 1130
CAACCCCTCTCTCCCGACCCAGAGGTNNAGTCCCGACCCCTCTTCCTCAGATCAGAGTCCCAAGTCC
1140 1150 1160 1170 1180 1190 1200
ACCTAGATTTTCCCTGNACACAGTGCCTCTGTGGNAGTTGACCAACCTTACAGTTGGTTTTCATTT
1210 1220 1230 1240 1250 1260 x
TTTNGTCCCTTTCCCTAGATCCAGAAATAAAGTTTAAGAGANGNCCAAAAA
AGGTTNATTCGCGCCTTGGCGTTATCGCTATCGCTACNCCNGTTCACCTTTTCCTTTTACCCCCCACA
670 680 690 700 710 720 x
ATTCCACGCCNACATPG
740 750

57. US-09-030-606-173 (1-1265)
US-09-020-747-34 Sequence 34, Application US/09020747

Initial Score	=	50	Optimized Score	=	231	Significance	=	0.23
Residue Identity	=	35%	Matches	=	257	Mismatches	=	459
Gaps	=	10	Conservative Substitutions	=			=	0

500 510 520 530 540 550 560
CTGAGGAGGTCTCGATAGACTCTATGACCCCTGTACCACCCAGCATGTTCTCGCGCGGAGGGCGAAG

[illegible]


```

570 580 590 600 610 620 630
ACCAAGAGGACTCTGCAAGGCTGACTCTGCGGGGCCCCCTGATCTGCAACGGGTACTTGCAGGGCCT----T
|||||
AACTCAAGGGGAGTGGAGCGTGAACCGTAAAGAGCCCAATCTTANCAAGTGGGGAANAGCTGGGTGACTCAAGC
30 40 50 60 70 80 90
640 650 660 670 680 690 700
GTGCTTTTCGAAAGCCCGTGTGGCCCAAGTGTGGCTGGCCAGTGTCTACACCAACCTCTGCAAAATCACT
|||||
TAGTTCTTGGAGCTCAACTTCTTGGCCCAACCAAGGACCAAGCTGACCAACAGCAGCTAAATCTTGGGCC
100 110 120 130 140 150 160
710 720 730 740 750 760 770
GAGTGGATAGAGAAACCGTCCAGCCAGTTAACTCTGGGACTGGGAACCCATGAATTTGACCCCAATA
|||||
GTGACTACTGGAGATCGGGCCCAATGGAGCATCTCCACGCAANGACATCCCT--CCTTCAGGCGCTACATG
170 180 190 200 210 220 230
780 790 800 810 820 830 840 850
CATCCTCGGAAGGAATTCAGGAATATCTGTTCACGCCCTCTCTCCCTCAGGCCAGGAGTCCAGGCCCC
|||||
GCCAGCTCAATCTACTACTTGTATTAANGAGCAGCTCCCGGAGTACAGCCTATATGACCAAGCTCTTG
240 250 260 270 280 290 300
860 870 880 890 900 910 920
AGCCCTCTCTCCCTCAAAACCAAGGTACAGATCCCGCCCTCTCTCCCTCA--GACCCAGGAGTCCAGACC
|||||
GGCTCAACCTCTCTCTCTGCTCCAGAACCGGGTGGCTGANTCCACAGGANTTGGANGGGTGGCT
310 320 330 340 350 360 370 380
930 940 950 960 970 980 990
CCCCAGCCCTCTCTCCCTCAGACCCAGGAGTCCAGCCCTCTCTCCCTCAGACCCAGGAGTCCAGACCCCA
|||||
GCCCAANGACATACANACCAATGCTACATCNACCAACAGGTCTCTGGAGCAATACATGATGGANGGAGCTA
390 400 410 420 430 440 450
1000 1010 1020 1030 1040 1050 1060
GCCCTCTCTCTCAGACCCAGGAGTGGAGGCCCAACCCCTCTCTCTCAGAGTCAAGTCCAGCCCC
|||||
CCNCAAGTNTCTCTGGCCNA--GGGTAACTCCCGCGGAGAGCTACACCTTCTTATTCACATCTCTGCTC
460 470 480 490 500 510 520
1070 1080 1090 1100 1110 1120 1130
CAACCCCTCTGTTCCCAAGACAGAGGTTNAGTCCAGCCCTCTCTCTCAGACCCAGGAGTCCAGTCC
|||||
GACACTATCAGGATGAATTCGCGG--GTTGCTCCAGAAAGCTTCAANAANATCTTTTCNCTGAAGGC
530 540 550 560 570 580 590
1140 1150 1160 1170 1180 1190 1200
ACCTAGATTTTCCCTGNACAGTGGCCCTTGTGGNAGTTGACCAACCTTACCAGTTGGTTTTCATTT
|||||
CCCGGATNCNTAGTACTAGATCGGCCCGCCATCGGTGGAGCTCCAACTTTCGTTNCCCTTTACTG
600 610 620 630 640 650 660
1210 1220 1230 1240 1250 1260 x
TTNGTCCCTTTCCCTAGATCCAGAAATAAGTTTAAAGAGANGCAAAAAA
|||||
AGGTTNATTTGCCCGCTTGGCTTATCATGTTACNCCNGTTCCTGTTGAAATNTTAAACCCCCACA
670 680 690 700 710 720 x 730
ATCCAGCCCNACATTNG
740 750

```

58. US-09-030-606-173 (1-1265)
US-08-806-596-36 Sequence 36, Application US/08806596
Initial Score = 50 Optimized Score = 253 Significance = 0.23
Residue Identity = 34% Matches = 283 Mismatches = 516

```

Gaps - - - - - 29 Conservative Substitutions - - - - -
40 50 60 70 80 90 100
CTGTCATGGAAGAAAGTAATCTTCTGCTCGGCGCTCTGGTGCATCCGAGTGGGTCTGTCTCAGCGGCACAC
|||||
CGGNCGCTTTTCGCGCGGCC
x 10 20
110 120 130 140 150 160 170
TGTTCAGAGAACTCTACACCATCGGCTGGGCTGACACAGTCTTGGAGCGCCAGCAAGAGCCAGGAGCCAG
|||||
CGTTTCATGACNAAGGCTCCTTCANGTTAAATACNNCTAGNNAACATTAATGGGTGCTCTCTACTAATAC
30 40 50 60 70 80 90
180 190 200 210 220 230 240
ATGTTGGAGGCGCCTCTCGTACGGCACCAGAGTACAACAGACCCCTTGTCTCTAACACCTCATG---
|||||
ATCATACNACAGTAGACCTGCGCCANACCGCACTCAGGCCATTCTACCAAGGAGAAAGGCTGGTCT
100 110 120 130 140 150 160
250 260 270 280 290 300 310
CTCATCAAGTTGGAGAAATCGGTGTCGAGTCTGACACCATCCGAGCATCAGCATTTGCTTCGCAAGTGCCT
|||||
CTCCACCCCTCTAGGAAGAGGCTCCCTTGTAAAGACACCAATNCGCTGAATCTNAAGTC--TTGTGTTT
170 180 190 200 210 220 230
320 330 340 350 360 370 380
ACCGGGGAACTCTGCTGCTGCTGGGTCTGCTGGGAGGCTGAGCTCAGGCTGCTGCTGCTG
|||||
ACTAATGGAAGAAATAAACAANAGGTTTGTCTCATGCTGGTCCGACCGAGCTGGCACTAAACAN
240 250 260 270 280 290 300
400 410 420 430 440 450 460
CCCTCTCAAGGAGTCTCTGCGCCAGTCCGCGGGGCTGACCCAGAGCTCTGCTGCCAGGAGAAATGCCTA
|||||
CCAGCGCTCACTCTGCTGGANAAATATTTCTTGTCTTTTGGACATCAGGCTTGATGTATCAGTCCCA
310 320 330 340 350 360 370 380
470 480 490 500 510 520
CCGTGCTCAGTGGGTG-----AACGTGCTGGTGTCTGAGGAGTCTGCAAGTAACTATGACCCG
|||||
CNTTCCACCCAGTGGCGNCCCTTCCCCATNTTGTGANTGANTGAGGCTGAAGCTTGAAGTCTGCTCA
390 400 410 420 430 440 450
530 540 550 560 570 580 590
CTGTACACCCAGCATGTTCTGCGCGCGGAGGAGCAAGACCAAGAGCTCTGCAACGCTGACTCTGGG
|||||
AAGTCTGCGCCACAAGACCGCCAGGAGGANGTNTTNCAGTGGATCTGC-----CAAN
460 470 480 490 500 510
600 610 620 630 640 650 660 670
GGGCCCCGTGATCTGCAACGGGTACTTGCAGGGCCTTGTGCTTTTCGAAAGCCCGCTGCGCAAGTTGGC
|||||
ANTACCNATCATCNNTGATATAAAGCGCCCTCAACGANATGCTTCCANCANCTTTAAGACCCATAATC
520 530 540 550 560 570 580
700 710 720 730 740
GTGCCAGTGTCTACCAACCTCTGCAAAATTCAGTGTGATAGAGAAACCGCTCCAGCGCAGTAACTC
|||||
CTNGAACCATGCTGCTCGGTCTGATCCNAAAGGAATGTTCTTGGGTCCCATCCCTCTTGTGTTNCTT
590 600 610 620 630 640 650
750 760 770 780 790 800 810
TGGGAGCTGGGAACCATGAATTAATGACCCCAATACATCTCTGGGAGAGGA-----ATTACAGGAATATCTGT
|||||
ACGTTGTTTGGACCCCTGCTNGATNATNACCAANTGANATCCCNAGAGACCCCTNCCCTGGCATTTGANT
660 670 680 690 700 710 720
820 830 840 850 860 870 880
TCCAGGCCCTCTCTCCCTCAGCGCCAGGAGTCCAGGCCCGCCCTCTCTCTCAACCAAGGAGTACAGA
|||||
TTCNTAATTTCTGCCCCCTACNNCTGAAGACACNATTCCTTNGGCGCCNCCNAGGNGAGTCAAGAGGTCTN
730 740 750 760 770 780 790 800

```


1010

890 X 900 910 920 930 940
 TCCCGAGCCCCCTCCCTCAGACCCAGGACTCAGACCCCGCCCTCTCTCCCTCAGACCC
 | | | |
 NGAAAAACCACNCN
 810 X

59. US-09-030-606-173 (1-1265)
 59. 09-030-606-173 sequence 16. Application US/08850713

Initial Score	=	50	Optimized Score	=	423	Significance	=	0.23
Residue Identity	=	37%	Matches	=	486	Mismatches	=	767
Gaps	=		Conservative Substitutions	=	37		=	0

TCCTCTACCGGGGAGACGACAGGTGTTCCGCCCCAATACCGAGGGGACACTGGAGGTGCTAGCAGTGAG
 310 320 330 340 350 360 370
 GG CAGCGCGCACTGCGACGCGCT
 X 10 20

GGCAGCGGCATGTGTCATGGAAACGAATTCTGTCCGCCCTCTGTGTCATCG--CAGTGGGTGT
| | | | | | | | | | | | | | | | | | | | | |
GACAGCCTGATGACCAGCTTCCTGCCAGCGCCCTAAGCCTGGAGCTCCCTCCCTAATGGACACCTGGGTGCT
380 390 400 410 420 430 440 450

100 110 120 130 140 150 160
GTCAGCGCACAGTGTTCAGAACTCCTACACATCGGGCTGGCGCTTCACAGTCTTGAGGCGGACCAAGA

[illegible][illegible]

TAGTGGCTTCCTGTTGCCAGGTGGCCCATCCTCGTTTAGGGGCTCCATGTCACCACTGAC
600 610 620 630 640 650 660

TTTCGcAGTGccocTAccGGGGGAActTTCcCTcCTTTCTGGCTGGGTCTGCtGGcAAcGGTgAGCTCAC
310 320 330 340 350 360 370

[illegible]

740 450 460 470 480 490 500 510
TCCAGGCGAATGCCGTACCGTGTGCGTGAACGTGTCGGTGTCTCTGAGGAGGTCTGCAGCTAAGC
|||||
TCCAGGCTCCCGCTCTCTTACGCCCCATGCGGGTGCCTGCTGTTGCTGC-CAAAT
820 830 840 850 860 870 880

520 530 540 550 560 570 580
TCTATGACCGCTGTACCAACCCACGATGTTCTGCGCGGAGGCGACAGACGAGTCTCTGCAACG
AATGTGCTCTGCTGCCACCTG-----TGTGCTGAGGTGCGTANTGCACAGCTGGGGGTGGGGC-

590 600 610 620 630 640 650 660
GTGACTCTGGGGGCCCTGATCTGCAACGGGTACTTCCAGGGCGTGTGTCTTCTCGGAAAAGCCCCCGTGTG
|||||
GTCCCTCTCTCTCTCCCCAGTCT -CTAGGGCTGCTGACTGGAGGCGCTCCAAAGGGGGGTTTCAGTCTCTGGAAG

670
 680
 690
 700
 710
 720
 730
 GCCAAGTTGGCGTGCCAGGTGTTACACCACTCTGCAATTCACGTGATAGAGAAAACCGTCCAGG
 TTATACAGGAGCCAGAGAGGCTCCATGCACTGGATGGCGGCACTCTCCAGGTGGATTACCCAGGCTCAG
 1020 1030 1040 1050 1060 1070 1080

740 750 760 770 780 790 800
CCAGTTAACTCTGGGACCTGGGAACCCATGAATTTGACCCCAATACATCTCGGAAGAAATTCAGGAAAT
-GGTTACACGTAGCTCTAGTTGAGACACACACCTAGAGAGGGTTTTGGGACCTCAATTAACCTCAGTCAC
1090 1100 1110 1120 1130 1140 1150

[illegible]

T---ACAGATCCCGAGCCCTCCTCCCTAGACCAGGAGTCCAGACCCGCCAGCCCTCTCCTCAGACC
| | | | | | | | | | | | | | | |
TGAAACATCCTCCATCGGAGTTTCACATATGAAGTATTTTGTAGGGAGAGGTCCTGTAGGGGCACACAC

[illegible]

1080 1070 1060 1050 1040 1030 1020 1010 1000 990 980 970 960 950 940 930 920 910 900 890 880 870 860 850 840 830 820 810 800 790 780 770 760 750 740 730 720 710 700 690 680 670 660 650 640 630 620 610 600 590 580 570 560 550 540 530 520 510 500 490 480 470 460 450 440 430 420 410 400 390 380 370 360 350 340 330 320 310 300 290 280 270 260 250 240 230 220 210 200 190 180 170 160 150 140 130 120 110 100 90 80 70 60 50 40 30 20 10

1090
1100
1110
1120
1130
1140
1150

CCACAGAGGTNNAGGTCCACGCCCTTCCNTCAGACCCAGCGGTCCAATGCCACCTAGATATTTTCCCTGNAC

1090
1100
1110
1120
1130
1140
1150

AGTAGAAGGAATCCATTCGTAGCTTTTCCTGTGTGTTGCTAATATTTGGGTAGGGTGGGGGATCCCCACAT

1160 1170 1180 1190 1200 1210 1220
ACAGTGGCCCTTG-----TGGNANGTTGACCAACCTTACAGTGGTGTTCATTTTNGTCCTTTT
1160 1170 1180 1190 1200 1210 1220
AATCAGTGGCCCTTGAGATACCTGGTTCATTGGCTGATCATTTGCCAGATCTCTTCCTGGGCTCGGCC
1200 1210 1220
1200 1210 1220

[illegible]

GGTTAGCGCTGTTGACGAGCGT
1670 1680

US-09-020-747-15	Sequence 155, Application US09020747				
Initial Score	=	49	Optimized Score	=	105
Residue Identity	=	38%	Matches	=	120
Conservative Substitutions	=	7	Mismatches	=	186
Gap	=			=	0
					0.22

740 AACTCTGGGACTGGGAACCCATGAATTGACCCCAATACATCTCTCGGGAAGGAATTCAGGAATATCT
750
760
770
780
790
800
ACTGGAATTAATAAACCCCA
X 10 20


```

820 830 840 850 860 870 880
TCCAGAGCCCTCTCCCTCAGGCCCA-GGAGTCCAGGCCCCAGCCCTCTCCCTCAAAACAGGGTACAG
||| ||| ||| ||| ||| ||| |||
TCACAGCTGTTGTCAAAGATCATCAGGGCATGGATGGAAAGTCTTTGGAACTGTAAAGTGCCTAACAC
30 40 50 60 70 80 90

890 900 910 920 930 940 950
ATCCCCAGCCCTCTCCCTCAGACCCAGGAGTCCAGACCCCCAGCCCTCTCCCTCAGACCCAGGAGT
||| ||| ||| ||| ||| ||| |||
ATGATCAGTATTTTGTATAATTTGAATACACGGTGCATACAAACTCTCTCCCTCTCTCTCTCTGGCC
100 110 120 130 140 150 160

960 970 980 990 1000 1010 1020
CCAGCCCTCTCTCCCTCAGACCCAGGAGTCCAGACCCCCAGCCCTCTCCCTCAGACCCAGGAGT
||| ||| ||| ||| ||| ||| |||
CCAGCCCCAGCCCTCAGACCTCACTGCTGTTCATCCAGGCCAGCATGTAGTGCTGATCTCTCTGG
170 180 190 200 210 220 230

1030 1040 1050 1060 1070 1080 1090
CCCCAACCCCTCTCTCTCAGAGTCCAGAGTCCAAAGCCCAACCCCTCTCTCCCTCAGACCCAGAGTNA
||| ||| ||| ||| ||| ||| |||
C-----TGCTTTAGCCCTCCANAAGTTTCTCTGAAGCCCAACCACTCTANGTGAAGGATGCTGCCCT
240 250 260 270 280 290 300

1100 1110 1120 1130 1140
GGTCCAGCCCTCTCTCCCTCAGACCCAGGAGTCCATGACCACCTAGATTTTC
||| ||| ||| ||| ||| |||
GGT
X

```

61. US-09-030-606-173 (1-1265)
US-08-904-809-20 Sequence 20, Application US/08904809

Initial Score = 49 Optimized Score = 216 Significance = 0.22
Residue Identity = 30% Matches = 234 Mismatches = 520
Gaps = 19 Conservative Substitutions = 0

```

300 310 320 330 340 350 360
GAGCATCAGCATGCTTCGCGAGTGCCTACCGGGGAACTCTTGCCCTGCTTCTGGCTGGGTCTGCTGGC
||| ||| ||| ||| ||| |||
TTTTTTTTTTTTTTTTTTT
X 10 20

370 380 390 400 410 420 430
GAAGGTGAGTCAAGGTGTGTCTCCCTCTCAAGGAGTCTCTGCGCAGTCCGCGGGGTGACCCA
||| ||| ||| ||| ||| |||
AAACCCCTCTCATTTAATGNAACTTCGAAATGTCCAAACCCCTCTCCAAATNCCNTTCCGGGNGG
30 40 50 60 70 80 90

440 450 460 470 480 490 500
GAGCTCTGCTCCAGGAGGAGTGCCTACCGTGTGCAAGTGTGCGTGTGCTGAGGAGTTC
||| ||| ||| ||| ||| |||
GGGTCCAAACCCCAANTTANNTTGGANNTTAAATTAATNTTNGGNNNAACCCNAATCTNANGAA
100 110 120 130 140 150 160

510 520 530 540 550 560 570
TCAGTAAGCTCTATGACCCGCTGTACACCCAGCATGTTCTGCGCGGGGAGGCAAGCAAGAGGAC
||| ||| ||| ||| ||| |||
AGTTNAACCCCAANTATNANC-----TTNAATNCCCTGGAACCCNGTNTTCCAAATNTTAAACCTTAANT
170 180 190 200 210 220 230

580 590 600 610 620 630 640 650
TCCTGCAACGCTGACTCTGGGGGGCCCTGTATCTGCAACGGTACTTTCAGGGCTTGTCTTCGGAATA
||| ||| ||| ||| ||| |||
CCCTCGGAATNGTNGGAAACCCCAANTTCTCNPAAGTGTGTTGAAGNTNAATNAACCCNCCA
240 250 260 270 280 290 300

660 670 680 690 700 710 720
GCCCGCTGTGCGCAAGTGTGGCGTGCAGGTCTTACACCAACCTCTGCAAAATCTACGTAGGTAGAGAAA
||| ||| ||| ||| ||| |||
ATTGTTTTNCCAGCGCTGAATTAATGGTTCGNTGTTTTTCNTTAAANAGGNNNCCCGGTTANT
310 320 330 340 350 360 370

```

```

730 740 750 760 770 780 790
ACCGTCCAGGCGAGTTAACTCTGGGACTGGGAACCCATGAAATGGACCCCAATATACCTCTCGGAAGA
||| ||| ||| ||| ||| |||
NAATCCCCCNCNCCCAATTAACCGANTTTTTTTTNGAATTTGGGANCNCNGGGAATTAACGGGNNNTCC
380 390 400 410 420 430 440

800 810 820 830 840 850 860
ATTGAGGAATATCTGTTCCAGCCCTCTCTCCCTCAGGCCAGGAGTCCAGGCCCCAGCCCTCTCCCTC
||| ||| ||| ||| ||| |||
CTNTTGGGGGCGNGNCCCCCTCCCTCGGGGTTNGGNCAGGNCNNAATTTGTTAAGGGTCCGAAAAATC
450 460 470 480 490 500 510 520

870 880 890 900 910 920 930
AAACCAAGGTTACAGATCCCGAGCCCTCTCTCTCAGACCCAGGAGTCCAGACCCCCAGCCCTCTCCCTC
||| ||| ||| ||| ||| |||
CCTCAGAAAAAANCTCCAG-----GNTGAGNTNGGTTTNCCTCCCTCCANGGCCCTCTCG
530 540 550 560 570 580

940 950 960 970 980 990 1000
TCAGACCCAGGAGTCCAGCCCTCTCTCTCAGACCCAGGAGTCCAGACCCCCAGCCCTCTCTCTCAG
||| ||| ||| ||| ||| |||
NANAGTTGGGTTTGGGGGCTGCGATTNTTTC-----CCTNTTNCCTCCCTCCCTCCCGGNGGANA
590 600 610 620 630 640 650

1020 1030 1040 1050 1060 1070 1080
CCAGGGGTTGAGGCCCCCAACCCCTCTCTCTCAGAGTCCAGAGTCCAAAGCCCAACCCCTCTCTCCCA
||| ||| ||| ||| ||| |||
GGTTNGTGTGTCNCCGCGCCNCAAGANTTTNCCGANTTAAATCTGCTNGGCGAAGT
660 670 680 690 700 710 720

1090 1100 1110 X 1120 1130 1140 1150
GACCCAGAGTNNAGTCCAGCCCTCTCTCTCAGACCCAGGAGTCCAAATGACCATAGATTTTCCTGNG
||| ||| ||| ||| ||| |||
CCNTGAGGNTTAAAGGCCCTCTNNCGG
730 740 750 X

1160
ACACAGTGC

```

62. US-09-030-606-173 (1-1265)
US-09-020-747-20 Sequence 20, Application US/09020747

Initial Score = 49 Optimized Score = 216 Significance = 0.22
Residue Identity = 30% Matches = 234 Mismatches = 520
Gaps = 19 Conservative Substitutions = 0

```

300 310 320 330 340 350 360
GAGCATCAGCATGCTTCGCGAGTGCCTACCGGGGAACTCTTGCCCTGCTTCTGGCTGGGTCTGCTGGC
||| ||| ||| ||| ||| |||
TTTTTTTTTTTTTTTTTTT
X 10 20

370 380 390 400 410 420 430
GAAGGTGAGTCAAGGTGTGTCTCTCCCTCTTCAAGGAGTCTCTGCGCAGTCCGCGGGGTGACCCA
||| ||| ||| ||| ||| |||
AAACCCCTCTCATTTAATGNAACTTCGAAATGTCCAAACCCCTCTNTCCAAATNCCNTTTCGGGNGG
30 40 50 60 70 80 90

440 450 460 470 480 490 500
GAGCTCTGCTCCAGGAGGAGTGCCTACCGTGTGCAAGTGTGCGTGTGCTGAGGAGTTC
||| ||| ||| ||| ||| |||
GGGTTCCAACCCCAANTTANNTTGGANNTTAAATTAATNTTNGGNNNAACCCNAATCTNANGAA
100 110 120 130 140 150 160

510 520 530 540 550 560 570
TCAGTAAGCTCTATGACCCCTGTACACCCAGCATGTTCTGCGCGGGGAGGCAAGCAAGAGGAC
||| ||| ||| ||| ||| |||
AGTTNAACCCCAANTATNANC-----TTNAATNCCCTGGAACCCNGTNTTCCAAATNTTAAACCTTAANT
170 180 190 200 210 220 230

580 590 600 610 620 630 640 650

```


[illegible]

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63. US-09-030-606-173 (1-1265)
   US-08-806-596-15 Sequence 15, Application US/08806596

Initial Score = 49 Optimized Score = 259 Significance = 0.22
Residue Identity = 39% Matches = 326 Mismatches = 450
Gaps          = 53 Conservative Substitutions = 0

      220       230       240       250       260       270       280
GAGTACACAGACCCTTGCTCGCTAACGCCCTCATGCTCATCAAGTTGGACGAATCCGTGTCGCAGTCTGCAC
                                     | | | | | | | | | | | | | | | | | | | |
      290       300       310       320       330       340       350
ACATCCGAGAGNCATCAGATTGCTTCGCAGTGCCTACCGGGGAACTCTTGCTCGTTCTGTCGTGGGT
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
ACTTGAAGGTACAACCCAGGAAACCCCTGGTGTGAGAGATGTGGAAACACAGATTTGGCGCTACTCGCGG
30 40 50 60 70 80 90
      360       370       380       390       400       410       420
CTGCTGGCGAAGGGTGAGCTCACGGGTGTGTCTGCCCTTTCAAGAGGAGTCCCTCTGCCCACTCGCGGGG

```

[illegible]

64. US-09-030-606-173 (1-1265) 24. Application US/09020747

Initial Score	=	49	Optimized Score	=	231	Significance	=	0.22
Residue Identity	=	3%	Matches	=	258	Mismatches	=	544
Gaps	=		Conservative Substitutions	=	20		=	0

120 130 140 150 160 170 180 190

[illegible]

```

5. US-09-030-606-173 (1-1265)
US-08-850-713-13 Sequence 13, Application US/08850713

Initial Score = 48 Optimized Score = 100 Significance = 0.20
Misidue Identity = 38% Matches = 104 Mismatches = 162
Gaps = 3 Conservative Substitutions = 0

800 810 820 830 840 850 860
TCAGGAATATCTGTTCCAGCCCTCTCCCTCAGGCCAGGAGTCAGCCGCCCTCTCTCCCTCAA
|||||
CACCCTCTTCTCTTGCCCGCAG

```

870 880 890 900 910 920 930
ACCAAGGTACAGATCCCA--GCCCTCTCTCAGACCCAGAGTCCAGACCCCGAGCCCTCCTCC
CCTGTTTNCCTCCACTTCCACTCCCTCTACTCTCTCAGACTGGCTGATGAGGCACTGCCCAAAATTN
30 40 50 60 70 80 90

940 950 960 970 980 990 1000
CTCAGACCCGAGGTCCAGCCCTCTCCCTCCCTCAGCCAGAGTCCAGACCCCGAGCCCTCCTCCTCCAG

[illegible]

AGCCACGAGCAGCAATTTCTGGT
| | | | |
AATTCACACAGAAACTCAGGAGCACCCCCT
240 250 260 x

1160
NACACAGTG

67. US-09-030-606-173 (1-1265)
US-09-071-710-12 Sequence 12, Application US/09071710

Initial Score	=	48	Optimized Score	=	101	Significance	=	0.20
Residue Identity	=	36%	Matches	=	106	Mismatches	=	187
Gaps	=		Conservative Substitutions	=			=	0

870 ACCAAGGTACAGATCCCGAGGCCCTTCTTCCTCAGACCAGGAGTCCAGCCCCCGCCCTCTCTCTCTC
950 960 970 980 990 1000 1010
AAGGCACCTGCCCAAAATTNNCCC X 10 20

[illegible][illegible][illegible][illegible][illegible]

[illegible][illegible]


```
660 670 680 690 700 710 720
TGCGCAAGTTGGCGTCCAGGCTGCTACACCAACCTCTGCAAAATTCACCTGAGTGGATAGAGAAACCGTCT
|||||
GGAGGCCAAGAGGCTCCATGCACTGGAATCGGGACTCTGAGGTGGATTACCCAGGCTCAGGTTTAAACAG
1020 1030 1040 1050 1060 1070 1080 1090
730 740 750 760 770 780 790 800
CAGGCCAGTTAACTCTGGGACTGGGAACCATGAATTTGACCCCAATATACATCTCGGGGAAGAAATTCAG
|||||
CTAGCTCTCTAGTTGAGACACACCTCAGAGAGGTTTTC-----GGAGCTGAATAAATCTCAG
1100 1110 1120 1130 1140
810 820 830 840 850 860 870
GAATATCTTTCCAGCCCTCTCCCTCAGGCCAGGATCCAGGCCCCAGCCCTCTCTCCCTCAACCA
|||||
TCACCTGTTTCCCATCTTAAGCCCTTAACCTGCAGCTTCGTTTAAATGATCTCTTCATGGGAGTTCT
1150 1160 1170 1180 1190 1200 1210 1220
880 890 900 910 920 930 940
AGGGT---ACAGATCCCCAGCCCTCTCCCTCAGACCAGGAGTCCAGACCCCCAGCCCTCTCCCTCA
|||||
AGGATGAACACTCTCTCATGGGATTGAACATATGAAGTTATTTCTAGGGAAGAGTCTCAGGGGCAAC
1230 1240 1250 1260 1270 1280 1290
950 960 970 980 990 1000
GACCCAGGAGTCCAGCCCTCTCCCTCAGACCAGGAGTCCAGACCCCCAGCCCTCTCTCCCTCC-----TCA
|||||
ACAAAGAACAGGTTCCCTCAGCCACAGCAGCTGTCTTTTGTGATCCACCCCTCTTACCTTTATCA
1300 1310 1320 1330 1340 1350 1360
1010 1020 1030 1040 1050 1060 1070 1080
GACCCAGGTTGAGCCCTCTCCCTCAGAGTCAGAGTCCAGAGTCCAGCCCAACCCCTCTCTCCCTCC
|||||
GGATGTGGCTGTGTGCTCTCTGTTGCCATCAGACACAGCAGCATTAATATTTAACTTTATTTATTA
1370 1380 1390 1400 1410 1420 1430
1090 1100 1110 1120 1130 1140 1150
CAGACCCAGAGTNNAGTCCAGCCCTCTCCCTCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAGAGTCCAG
|||||
ACAAAGTAGAGGAAATCCATCTGTTGCTCTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG
1440 1450 1460 1470 1480 1490 1500
1160 1170 1180 1190 1200 1210
GNACACAGTCCGCTCTG-----TGGNAGTTGACCACTTACCACTTACCACTTACCACTTACCACTTAC
|||||
CAACAATCAGTCCCTGAGATAGTGGTCAATGGCTGATCATTCAGCAATCTCTCTCTCTCTCTCTCTCTCT
1510 1520 1530 1540 1550 1560 1570 1580
1220 1230 1240 1250 1260 1270
TTTCCCTTAGATCAGAAATTAAGTTTAAGAGNGNCAAAAAA
|||||
GCCCCCAATGCTCAACCCAGGACCTTGGAATTTCTACTCATCCCAATGATTAATTCCTCAATGCTGTTAC
1590 1600 1610 1620 1630 1640 1650
CCAAGTTAGGTTGTTGAAGGAT
1660 1670
74. US-09-030-606-173 (1-1265)
US-09-071-710-16 Sequence 16, Application US/09071710
Initial Score = 48 Optimized Score = 429 Significance = 0.20
Residue Identity = 37% Matches = 487 Mismatches = 767
Gaps = 37 Conservative Substitutions = 0
X
GGAGCCCGCACTCGAGCCCT
10 20
TCCCTCTACACCGGAGGAGCAGGTGTTCTGCCCCAAATACCAGGGGACACTGAGAGTCTAGCAGTGA
310 320 330 340 350 360 370
30 40 50 60 70 80 90
GGCAGCGGCACCTGCTCATGGAACAGATTGTTCTGCTGGGGCTCTCTGTTGATCCG--CAGTGGGTGCT
```

```
|||||
GACGCTGATGACAGCTTCTGCGAGGCCCTAAAGCCTGGAGTCCCTTCCCTAAAGACACAGTGGTCT
380 390 400 410 420 430 440 450
100 110 120 130 140 150 160
GTGAGCGCACACTGTTTCCAGAACTCTTACACCATCGGCTGGGCTGACAGTCTTTGAGCGCGCAACAGA
|||||
GGAGGAGTGGCTGCTGCCACATC-CACCCCGGCTCTCGGGGGCTCTGCTGATGATCTCCGTAGTCTGT
460 470 480 490 500 510 520
170 180 190 200 210 220 230
GCCAGGAGCCAGATGTGAGGCCAG---CCTCTCCGTACGACCCAGAGTACAAACAGACCTTGTGTCGC
|||||
GGTGGTGGTGGAGCCACCGAGCGAGGGTGGTTCGGCGCGGGGATCTGCTGACCTGACCTGCCATCTGGA
530 540 550 560 570 580 590
240 250 260 270 280 290
TAAGACCTCATGCTCATGAGTTGGACGAATCCGTGTCGAGTCTGACACCATCCGAGCATC-----AG
|||||
TAGTGCCCTTCTGCTGCCAGGTGGGCCCATCCCTGTTATGGGCTCCATGTTCCAGCTCAGCCAGTCTGT
600 610 620 630 640 650 660
300 310 320 330 340 350 360 370
CATGCTTTCGAGTCCCTACCGCGGGGAATCTTGCCTCTGCTTCTGGTGGGCTGCTGCGGACAGGTGA
|||||
CACTGCCCTATGATGCTGCTGCCAGGCTGGGCTGCTGCTGCCATTTACTTTGCTACACAGTATGATTGA
670 680 690 700 710 720 730
380 390 400 410 420 430 440
GCTCAGGGTGTGCTGCTGCCCTCTTCAAGGAGTCTCTGCCCCAGTCCGGGGCTGACCCAGAGCTCTGC
|||||
CAAGAGGACTGGCCAAATACTAGCGTAGAAATTTCCAGACATTTGGGGTGGAGGGCTGCTCTCATCTGG
740 750 760 770 780 790 800 810
450 460 470 480 490 500 510
GTCCAGGAGCAGAAATGCTGCTGAGTGGGCTGCGGGCTGCGGCTGCTGCTGCTGCTGCTGCTGCTGCTG
|||||
GTCCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT
820 830 840 850 860 870 880
520 530 540 550 560 570 580
CTCTATGACCCGCTTACACCCAGCATGTTCTGCGCGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
|||||
TAATGTGGCTCTCTGCTGCACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
890 900 910 920 930 940
590 600 610 620 630 640 650
GGTCACTCTGGGGGCGCTGATCTGCAACGGTACTTGCAGGGCTTGTGCTTTCGGAAGAGCCCGTCT
|||||
CGTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
950 960 970 980 990 1000 1010
660 670 680 690 700 710 720 730
GGCCAACTTGGCGTGGAGTGTCTACCAACCTCTGCAATTTCACTGAGTGGATAGAGAAACCGTCCAG
|||||
CTTATACAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
1020 1030 1040 1050 1060 1070 1080
740 750 760 770 780 790 800
GCCAGTTAACTCTGGGAGTGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
|||||
G-GGTTAACTAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
1090 1100 1110 1120 1130 1140 1150 1160
810 820 830 840 850 860 870
TATGTTTCCAGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
|||||
CCTGTTTCCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
1170 1180 1190 1200 1210 1220 1230
GT---ACAGATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
|||||
GT---ACAGATCCCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG
|||||
```


CTCTATGACCCCGCTGTACCACCCCCAGCATGTTCTGGGCCCGCGGAGGGGCAAGAACCCAGGAGGAGTACGACG

AGGTTAGGGTCTTGAAGGAAGGT
1670 1680

Initial Score	=	47	Optimized Score	=	81	Significance	=	0.13
Residue Identity	=	43%	Matches	=	96	Mismatches	=	.119

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GGGGGTCAATTTTCATGGGTTCACAGAGTTAACTGGCGTGGACGGTTTCTCTATCCACTCAGTGA

640 650 660 670 680 690 700 710

[illegible]

13. US-09-030-606-173 (1-1263)
US-08-806-596-18 Sequence 18, Application US/08806596

Initial Score	=	57	Optimized Score	=	246	Significance	=	1.94
Residue Identity	=	33%	Matches	=	275	Mismatches	=	522

16. US-09-030-606-173' (1-1265)
US-09-020-747-11 Sequence 111, Application US/09020747

Initial Score =	57	Optimized Score =	256	Significance =	1.94
Residue Identity =	36%	Matches =	298	Mismatches =	496
Gaps	=	24	Conservative Substitutions	=	0

Initial Score = 57 Optimized Score = 256 Significance = 1.94
Residue Identity = 36% Matches = 298 Mismatches = 496
Gaps = 24 Conservative Substitutions = 0

Initial Score = 57 Optimized Score = 256 Significance = 1.94
Residue Identity = 36% Matches = 298 Mismatches = 496
Gaps = 24 Conservative Substitutions = 0

Initial Score = 57 Optimized Score = 256 Significance = 1.94
Residue Identity = 36% Matches = 298 Mismatches = 496
Gaps = 24 Conservative Substitutions = 0

Initial Score = 57 Optimized Score = 256 Significance = 1.94
Residue Identity = 36% Matches = 298 Mismatches = 496
Gaps = 24 Conservative Substitutions = 0

Initial Score = 57 Optimized Score = 256 Significance = 1.94
Residue Identity = 36% Matches = 298 Mismatches = 496
Gaps = 24 Conservative Substitutions = 0

Initial Score = 57 Optimized Score = 256 Significance = 1.94
Residue Identity = 36% Matches = 298 Mismatches = 496
Gaps = 24 Conservative Substitutions = 0

Initial Score = 57 Optimized Score = 256 Significance = 1.94
Residue Identity = 36% Matches = 298 Mismatches = 496
Gaps = 24 Conservative Substitutions = 0

Initial Score = 57 Optimized Score = 256 Significance = 1.94
Residue Identity = 36% Matches = 298 Mismatches = 496
Gaps = 24 Conservative Substitutions = 0

[illegible]

100	110	120	130	140	150	160	
1060	1070	1080	1090	1100	1110	1120	
GGTGGCGTACGGAGAGCGCTGCACCATCTGGCTCCCTGCTCTTGGTCGGCCCTCAAGACTGTGCAGGC							
111	111	111	111	111	111	111	
ACGGCCTATCACTGCATTGCCCTTACTCAGGT-GCTACCGGACTCTGG---CCCCTGATGCTGTGATTTTC							
170	180	190	200	210	220	230	
1130	1140	1150	1160	1170	1180	1190	1200
CCAGCCCGATGGTGTAGGAGTTCGTGAAACAGTGTGGGGCTGACAGCACCATCTGCCGATGACCAGGACGC							
111	111	111	111	111	111	111	111
ACAGGATGCCCTATTGTCTCTTACACCCACAGGGCCCTACTCTCTCGGATGTGTTTTTAATAATATGTCA							
240	250	260	270	280	290	300	
1210	1220	1230	1240	1250	1260	X	
CGGAGCAGAACAAATTCGTTTC---CATGACCAGTGGCGCTGCCAGGCGCTGCAGTGGCGGCTGCC							
111	111	111	111	111	111	111	111
GCTATGTGCCCACTCTCTCTTCAATGCCTCCCTCCCTTCCCTACCACTGCTGAGTGGCCCTGGAACTGTGTTTA							
310	320	330	340	350	360	370	
AACTGT							
380							

ACGTTTCACGCACTGCAGCAGCGTAGGCATTCTGCCTGGGACGCAGAGCTCTGGGTGCAGCCCCCGCAGCTGGG

[illegible]

25. US-09-030-606-173' (1-1265)
US-09-030-606-173' sequence 109. Application US/09020747

Initial Score	=	53	Optimized Score	=	290	Significance	=	1.66
Residue Identity	=	36%	Matches	=	326	Mismatches	=	553
Gaps	=		Conservative Substitutions	=	21		=	0

[illegible]

24. US-09-030-606-173' (1-1265)

US-09-030-806-173 (1 1203)
US-09-020-747-13 Sequence 135, Application US/09020747

Initial Score	=	53	Optimized Score	=	121	significance	=	1.66
Residue Identity	=	36%	Matches	=	132	Mismatches	=	218.
Gaps	=		Conservative Substitutions	=	0		=	0

[illegible]

660 670 680 690 700 710 720
TCAGGGCCCCCAGAGTACCGTTGCAGGAGTCCCTTGCTGTCTGCCCTCCGGCGGCAGAACATGCTGG
||||| ||||| ||||| ||||| ||||| ||||| |||||
TCAGAATCCCTCCAAAGAAATCATG-----ATAATCTTATACCATANCAGTGGTGACTGGTTTAAGCG

GGTGGTACAGGGGTCATAGAGCTTACTCGACAGCTCTCTCAGACACACCACGACAGCTTCAGCGACTCGACCA

CGGTAGGCATTCTGCTGGGACGACAGACTCTGGGTCAAGCCGCCCGCAGCTGGGCAGAGGACCTCTCTTGGAAGA
TACACNCCTAGCANCTGTAATTCACAGGTGGCCCCCAACTCTCTGACGCGGTCTCTGTGCCAGNCCCTGNAAG

CAGTCCCTGGAATTGGATACCACTGCAGCGGTTC

720 730 740 750 760 770 780
 CAGAACTGCTGGGGTGGTACAGCGGGTCTATAGAGCTTACTGACAGCTCTCAGACACACCCACGACGTTG
 TTTGCTCAAGCTGGGCTACTTCCCTCATCGCAGCCGGCGT--TGTGGTCTTTTCTCTTGGTTTCTTGGCTGCTGCT
 290 300 310 320 330 340 350
 790 800 810 820 830 840 850
 ACGCACTGCAGCAGCGTAGGCATTTGCTGGGACGAGAGCTCTGGGTACGCCCGCCGCGACTGGCGAGAGG
 ACCCTCTTTGAAGAGGGGAGACACACACCGGTGAGCTCACCGTTCCGACGAGAGACCCAGCAGAAACAGGAGG
 ATGGTGTAGACAGCGAGAGCAAGTGTGCCCTCGTGAGCTTCTTTCATCTCTCTCTCATCTTCATTCATTCGCTG
 360 370 380 390 400 410 420
 A---AGTTGAGCTGCTTGGTCCGCTGGTGTACACCACAATGGCTGAACCATTCCTGAGCTTCTGAGTTGCTGGTAN
 430 440 450 460 470 480 490
 860 870 880 890 900 910 920 930
 AAGAGTTCCCGCGGTAGGGCAGTCCGAAGCAATGCTGATCTCCGGATGGTGCAGACTCGGACACAGCAATT
 TGGCTGCCATCAANAAGATTATGGGTTCGCCAGGAAATTCACCTCAANTGTGAAACACCCNCCATGAAGAAGG
 500 510 520 530 540 550 560
 1010 1020 1030 1040 1050 1060 1070
 CGTCCAACTTGATGAGCATGAGTTCGTTAGCGACCAAGGGT-CTGTGTACTCTGCGTGCCTACGGAGAGG
 TTTTCTTTTCTGTTGCTTCCCAACTATACCGGAATTTTGAAGANTCCCTACTTCTCAAAAANAANAANA
 570 580 590 600 610 620 630
 1080 1090 1100 1110 1120 1130 1140
 CTGGCTCCCACTGCTGGCTCCCTGGCTTGTGGTGGCTCAAGACATGTGCAGCCCGCGAGCAGAACTTGGTGTAG
 TTTTCTTTTCTGTTGCAATGAACACNTCCCAANACGCCAATNAAACCTGCCCNCCNCAAA
 640 650 660 670 680 690 700
 1150 1160 1170 1180 1190 1200 1210
 GAGTCTGGAAACAGTGTGGCTGACAGCACCCACTGCGGATGCACAGAGCAGCCGAGCAGAACTTGG
 TTTTCTTTTCTGTTGCAATGAACACNTCCCAANACGCCAATNAAACCTGCCCNCCNCAAA
 710 720 730 740
 AAGTNCNCAACAAAAAANTNNAAGGTTN
 1220
 TTTTCCATGA

US-09-030-606-173' (1-1265)
 US-09-020-747-17 sequence 174, Application US/09020747

Initial score = 52 Optimized Score = 405 Significance = 1.59
 Residue Identity = 35% Matches = 453 Mismatches = 808
 Conserved Substitutions = 0

x 10 20
 TTTTCTTTTCTGCTTTCTTTA
 TTTTCTTTTCTGCTTTCTTTA

100 110 120 130 140 150 160
 GATGGTGGAGCCAGCCTCTCCGTACGGCAGAGTACAAAGACCCCTTGTCTGCTAACGACCTCATGCTGCT
 170 180 190 200 210 220 230 240
 30 40 50 60 70 80 90
 AACTTTATTTCTGATCTAGGGGAAGGACNAAAATGAAACCACTGGTAAGGTTGGGTCAACNTNCC
 CATCAAGTTGACCAATCCGTGTCCGAGTGTGACACCATCCGGAGCATCAGCATTTGCTCCAGTGGCCCTAC
 170 180 190 200 210 220 230 240
 100 110 120 130 140 150 160
 ACAAGGGGCGACTGTGNCAGGAAATCTAGTGGCATTTGACCNCTGGTCTGANGAAGAGGGGCTGGG
 TTTTCTTTTCTGTTGCAATGAACACNTCCCAANACGCCAATNAAACCTGCCCNCCNCAAA
 250 260 270 280 290 300 310
 CGCGGGAACCTTTCCTGTTTCTGGCTGGGGTCTGCTGGCGAAGCGGTGAGCTCAGGCTGTGTCTGTCTGCTG

Initial Score	=	52	Optimized Score	=	405	Significance	=	1.59
Residue Identity	=	35%	Matches	=	453	Mismatches	=	808
Gaps	=	33	Conservative Substitutions	=			=	0

[illegible]

[illegible][illegible]

28. US-09-030-606-173' (1-1265)
US-09-030-606-38 sequence 38. Application US/08806596

Initial score	=	51	Optimized Score	=	200	Significance	=	1.52
Residue Identity	=	29%	Matches	=	222	Mismatches	=	502
Cons	=	33	Conservative Substitutions	=			=	0

ATCTAGTGGCATTGGACNCCTGGGCTCTGGAAGAGGGGTGGGACCTNNACCTCTGGGCTCTGGGAACG

AGGGGTGGGGCTTGGACCTCTGACTCTCAAGAGGAGGGGTGGGGGCTCAACCCCTGGGTCTGAGGGA
 TTTTGTGTTTAAAAACCCCTCCATGTAATGAACCTTCGNAATTTGTCCAACCCCTCCNCCGAATNN
 200 210 220 230 240 250 260
 270 280 290 300

GGAGGGGCTCGGGGGCTCGGACTCCTGGGTCTGANGAGGAGGGCTGCACCTCTGGTCTCAGGAGCAGAG,
 270 280 290 300 310 320
 GAGG | | | | | | | | | | | | | | | | | | | | | | | | | | | |
 CCATTCGCGGGGGGGTGCCAAACCACAATAATTATTTTGA-----NTTAAATTAATNTT
 100 110 120 130 140 150

GGCTGGGGGCTCTGGACTCCTGGGTCTCAGGGAGAGGGCTGGGATCTGTACCCCTTGGTTTGAGGGAGGA
 340 350 360 370 380
 NATTTGGGGGAANAACCAATCTNAGAAATTTTACCCATTATTAACCTTAAATNCTNGAAACCCNTGGNT
 160 170 180 190 200 210 220

10 420 430 440 450 460 470 480 490 500
 GGGGCTGGGGCCGTGACCTCTGGGCTGAGGAGAGGGCTGGGACACAGATATTCCTGAATTCCTCCGG
 TCCAAAATTTTAAACCCCTTAATCCCTCGAAATGNTAANGAAACCAAAATTCNCTAAGGCTNTTGA
 230 240 250 260 270 280 290

AGGATGTATTGGGGTCAATTTTCATGGGTTCCAGTCCCAGAGTTAACTGGCGCTGCACGGTTTCTCAT
 ||| |||| | | | | |
 AGGTTNGATTAAACCCCTTTNANTTTTTNACCNNGNCTNAANTATTNGNTCCGGTGTTTCCCTTT

CCACTCAGTGAATTTGCAGAGGTTGTGTGTAGACCTTGGACGCGCCACATCTGGCCACAGCGGGGTTTTCGCTT
AANCNTGGTGACTCCC-----GNTATGAANNCCGTANCCATTAACCGAATTTTTTTTGAATTGGAAA
370 380 390 400 410 420 430

440	450	460	470	480	490	500	100	110	120	130	140	150	160
GAGGAGGAGGGCTGGGAACAGATATTCCTGAATTCCTCCGAGGATGATATTTGGGGTCAATTTCAATGG													
CACCTACCTGTTCCAGCTGACAGTGACTAGCTCAGACCAACCACAGAGGA-----CACGGCCAACGTCACAG													
170	180	190	200	210	220								
510	520	530	540	550	560	570	580						
GTGCCAGTCCCCAGAGTTAACTGGGCTGGAGGGTTTCTCTATCCACTCAGTGAATTTGCAGAGTTGGTG													
--TCAGTGTGCTGCCACCAAGCAGACAGAGAAGACTACTGCTTCGCATCCAAACAANFTGGTGCTGCCGGGG													
230	240	250	260	270	280	290							
590	600	610	620	630	640	650							
TAGACACCTGGCAGCCCAACTTGGCCACACAGGGGGTTTCCGAAAGACACAAAGCCCTCGAAGTACCCTGTG													
CTCTTTCCCAACGCTGCTATGACCCACGAGCAGAGATCTCCAAAGATTTCTGTTATG-----G													
300	310	320	330	340	350								
660	670	680	690	700	710	720							
CAGATCAGGGGCCCCCAGAGATCACCGTCTCCAGAGTCTCTTCTGCTCTCCGCGCGGCACGAACATG													
AGCTGCTTTGGCAACAAGAACTACCTTCCGGGAAGAGTAGTGCATTTCTANCTGTCTNGSGTGTGCACAGG													
360	370	380	390	400	410	420							
730	740	750	760	770	780	790							
CTGGGTGGTACAGCGGGTCATAGAGTTACTGCAGACCTCTCTCAGACACACACAGCTTACACGCAGCTGC													
TGGGCGCTTTGANAGCANCTCTGGGGCTCANGCGACTTTCCCGCAGGGCCCTCCATGTGAAGGCGCCATCC													
430	440	450	460	470	480	490							
800	810	820	830	840	850	860							
AGCAGGTAGGCATTCGCTGGGACGACAGAGTCTGGGTACGCCCCCGCGACTGGGACAGGAGCCTCTCGG													
ANTGTTCTTGGCACTGTGC-AGCCCCACAGTTCCGCTGCANCAATGCTGCTGCATCNACANTTTCCTTNG													
500	510	520	530	540	550	560	570						
870	880	890	900	910	920	930	940						
AAGAGGCAGACACACACCCGTTAGCTCAGCGTTGGCAGCAGCACGCCACCCAGAAAGAGGAGAGATGCC													
AATTGTGACACACCCCCANTGGCCCCCAACCCCTCCCAACAAAGCTTCCCTGTTTNAAAATATACNCCANTTGG													
580	590	600	610	620	630	640							
CGCGGTAGGCGACTGCGAGCAATGCTGATGCTCCGGATGGTGTAGACTCGGACCGGATTCGTCCAATCT													
CTTTTNCACAAACCCCGGCCCTCCNTTTTCCCNNTNACAAAGGCGCTNGCTTTTGAAGTGCCTGCCNNAAC-													
650	660	670	680	690	700	710							
1020	1030	1040	1050	1060	1070	1080							
TGATGAGCATGAGGTCTGTAGCAGCAGAGGGTCTGTTGTAATCTGGTCCGCTACGAGAGGCTGGCTCCA													
---CCNGAACTTCCNNGGAAAAANTNCCCGCTGTTCTTNNANCCCTCCCNCAAANCTNCCCGCC													
720	730	740	750	760	770	780							
X 1090	1100	1110	1120	1130									
CCATCTGGCTCCCTGGCTCTTGTCGGCTCAAGACTGTGCGGCCCGAC													
C	C	C	C	C									
X	X	X	X	X									

Initial Score	=	51	Optimized Score	=	257	Significance	=	1.52e-06
Residue Identity	=	37%	Matches	=	302	Mismatches	=	480
Gaps	=	33	Conservative Substitutions	=			=	0

[illegible]

33. US-09-030-606-173' (1-1265)
 US-09-020-747-13 Sequence 131, Application US/09020747

Initial Score	=	50	Optimized Score	=	116	Significance	=	1.45
Residue Identity	=	38%	Matches	=	137	Mismatches	=	195
Gaps	=	27	Conservative Substitutions	=			=	0

780	790	800	810	820	830	840	850	860	870
ACACGTTACGCACTGCGACGAGTAGGCATCTGCGTGGACGACGAGCTCTGGGTGACGCCCCCGGAGCTG									
								CTTTTTGAAAGATCGTGTCCAC	
								X	
								10	20

860	870	880	890	900	910	920
GGCAGAGGACCTCCTTGAAGAGGGCAGACACACACCGGTGAGCTCACCGTTCGCCAGCAGACCCAGCCAGACA						
TCCTGTGACATCTGTGTTTAATGAGCTTTCCCATGCAGTANGACTGSTATGTTGCAGCTGTCCAGATAAA						
30	40	50	60	70	80	90

930	940	950	960	970	980	990
AACGAGGCAAGAGTTCCCGCGGTAGGCACTGCGAAGCAATGCTGATGCCGATGGTCTCAGACTCGGA						
ACATTTGAGAGCTCCAAATAGAGCTTCTCCAGGTTCCGCTGCTGCTCC						
100	110	120	130	140	150	160

1000	1010	1020	1030	1040	1050	1060
CACGATTCGTCCTGCAACTGATGAGCATGAGTCCCTTAGCGAGCAAGGTCTGTTGTACTCTGGGTGCCGTAC						
CTCTTTAGGAGGCATCTCTGAACCTAGATTAAGCAGCTGTGAA						
170	180	190	200	210	220	

1070	1080	1090	1100	1110	1120	1130
GGAGAGGCTGGCCTCCACCACTCTGGCTCCCTGGCTCTTGGTGGCGCTCAAGACTGTGCGAGCCAGCCGCGAT						
-----TTTATTATCCAACTTAACCTTCCATCTGTTATCATCTGGAGAAAGCCAGACTCCCCANGAC						
230	240	250	260	270	280	

1140	1150	1160	1170	1180	1190	1200	1210
GGTGTAGGAGTTCGTGGAACAGTGTGGCGGTGACAGCAGCACCCACTGCGGATGCACCGAGCCCGGAGCAGA							
NGGTACGATTTGGGATANAAGGATTTGGTGAAGCTGGCGTTGTGGT							
290	300	310	320	330	X		

1220	1230
CAATTCGTTTTCCATGACCAGTGCCGC	

34. US-09-030-606-173' (1-1265)
 US-08-806-596-40 Sequence 40, Application US/08806596

Initial Score	=	50	Optimized Score	=	226	Significance	=	1.45
Residue Identity	=	38%	Matches	=	265	Mismatches	=	440
Gaps	=	27	Conservative Substitutions	=			=	0

490	500	510	520	530	540	550	560
TTTTGGGGTCAATTTTCATGGGTTCCAGTCCCGAGAGTTAACTGGCTGGACGGTCTTCTATCCACTCAG							
						GTGGTATTTTCTGTGAAGTCA	
						X	
						10	20

570	580	590	600	610	620	630
TGAATTTGCAGAGGTTGGTGTAGACACTGGCAGCCCAACTTGGCCACAGGGGCTTTTCGAAAGACACACA						
GTGTTCTCCCTCGTAGGTTAGGAAACACCCCTCATAGTGAACCC						
30	40	50	60	70	80	90

640	650	660	670	680	690	700

1220
 TCGTTTCCATGA
 170 180 190 X
 TCCTCCTCAGGTGCGTANTGCACAGCTGGGGCTG
 1150 1160 1170 1180 1190 1200 1210
 TAGGAGTTCTGGAACAGTGTGGCGCTGACAGCACCCACTCGCGATGCCAGGAGCCCGCAGCAGCAAT
 1080 1090 1100 1110 1120 1130 1140
 AGGCTGGCTCCACCATCTGGCTTCCTGCTCTTGGTGGCGCTCAAGACTGTGAGGCCACCCCGATGCTG
 30 40 50 60 70 80 90
 AAAAAATTCCAGCACAATTGGGGTGGAGGGCTGCCTCACTGGTCCCAGCTCCGCCGCTCCTCTTTAGCCCAAT

36. US-09-030-606-173' (1-1265)
 37. 00 525-307-6 sequence 6
 Application US/09525397

US-09-030-606-173, (1-1265)
US-09-525-397-6 Sequence 6, Application US/09525397

Initial Score	=	49	Optimized Score	=	76	Significance	=	1.38
Residue Identity	=	40%	Matches	=	82	Mismatches	=	113
Gaps	=		Conservative Substitutions	=	6		=	0

930 940 950 960 970 980 990
AGGCAAGATTCCCCCGGTAGGCGACTCGGAAGCAATGCTGATCTCGGATGGTGTTCAGACTCGACACG
CTTGCCCAATACTACGCGTAG

1000 1010 1020 1030 1040 1050 1060 1070
GATTCGTCACACTTGATGACATGAGTCGTTAGCGACAGGCTCTGTGTACTCTGGTCCCGTAGCGGAG

AAACCTCCAGCACATTTGGGGTGGAGGGCGCTGCATCTGGGTCCCAGCTCCCGGCTCTGTAGCCCCATG

AGGTGGCTCCACATCTGGCTCCTGGCTCTTGGTCGAGGCGCCACGCCGATGGT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GGGTG-----CGGGCTGGCGGCCAGTTCTTGCTGCACAAGTAATGTGGCTCTCTGCTGCCACCCTGT

1150 1160 1170 1180 1190 1200 1210
TAGGAGTTCTGGAAACAGCTGCGCGCTGACAGACCCACTGCGGATGCACAGGAGCGCCGAGCAGACAT
TCCCTGCTCAGGTGCGGTANTGCACAGCTGGGGGCTG

1220
TCGTTTTCCATGA

77. US-09-030-606-173' (1-1265)
US-09-841-894A-6 Sequence 6, Application US/09841894A

Initial Score =	49	Optimized Score =	76	Significance =	1.38
Residue Identity =	40%	Matches =	82	Mismatches =	113
Gaps	=	6	Conservative Substitutions	=	0

AGCGAAGAGTTCCCGCGGTAGGGCACTCGGAAGCAATGCTGATGCTCCGGTGGTGTGAGACTCCGACACACAC

0000 GATTGTCGAACCTTGATGACATGAGGTCGTTAGCGACGAGGGTCTGTCTACTCTGGGTGCGGTACGGA

AAAAC TTCAGCAGCACATTGGGGTGGAGGGGCTGCCCTCACTGGGTCC CAGATCCCCCGCTGCAGTTTC

30 40 50 60 70 80 90

GGCGCTGGGGGCTCGATCCTCGGTCTGTGANGA-GGAGGGGTGGACTCCTGGGTCTGAGGGAGGAGGGGG
||| || | | | | | | | | | | | | | | | |
GGGWTCACCTTTCAGCCCTGCAGATCCTTGCCCTACACACTGGCCTCCTACCACGGGGGAAGAAGCAGGTG

270 280 290 300 310 320 330

GGGCTGGGGGCTGGACTCCCTGGCTCTGANGGA-GGAGGGCTGGACTCTGGGTCTGAGGAGGAGGGG

44. US-09-030-606-173' (1-1255)
US-09-020-747-71 Sequence 71, Application US/09020747

Initial Score	=	48	Optimized Score	=	144	Significance	=	1.31
Residue Identity	=	27%	Matches	=	148	Mismatches	=	381
Gaps	=		Conservative Substitutions	=			=	0

GGTGTAGACACTGGCACC GCCCACTTGGCCACACG GGGGCTTTTCGAAAGACACA GAGGCCCTGC AAGTACCC

580 590 600 610 X 620 630 640

GGTGTCCCAGTCCCCAGAGTTAATACATGGCGCTGGACG GTTTCCTCATCCACTCAGTGA -ATTTCGACAGGTT

510 520 530 540 550 560 570

|| || || || || || |

GGTGCGCATCACCCCATNAAGGGAACACATTTGANTTTTTTTTTCNCATATTTTAAATTACNACCAGAATAATTC

390 400 410 420 430 440 450

[illegible]

[illegible]

[illegible]

56. US-09-030-606-173' (1-1265)
Application US/08806596

Initial Score	=	45	Optimized Score	=	242	Significance	=	1.11
Residue Identity	=	36%	Matches	=	298	Mismatches	=	478
Gaps	=		Conservative Substitutions	=			=	0

[illegible]

160 170 180 190 200 210 220

620 630 640 650 660 670 680

GGGCTTTTCCGAAAGACACAAGAGCCCTGCAAGTACCCGTTGCAGATCAGGGGCCCCCAGAGTCAAGCTTGC

-GTTTATTNTCCAGCNCCTNCCNACCCCTACNTCTTCNNAGCTGTGTCNNACCCCTNGTCNCGNACCCCGCN

230 240 250 260 270 280 290

690 700 710 720 730 740 750

AGGAGTCCTCTTGCTTGGCTTCGCCCTCGCGCGGCGACAGATCTGCGGTGTGTCAGCGGGTGCATAGAGCTTAC

111 111 111 111 111 111 111

AGGTGGGATCGGGTTTNNNTTACCGNGNCCCTCTCCGCCCTTCATNACGANCNCCGACACACACCNAN

300 310 320 330 340 350 360

760 770 780 790 800 810 820

TGAGACCTCTTCACACACCACCGACAGTTTCACGCACTGCAGCACCGTAGGCAATTCGCTGGGACGAGCA

111 111 111 111 111 111 111

NGCNGCNCGCCGNNCTCTTGCCNCCCTGTCTTNNCCCTGTNGCCTGGCNCNGNACCGCATTCGACCTC

370 380 390 400 410 420 430

830 840 850 860 870 880 890

GCCTGGGTGAGCCCCCGGACCTGGCGAGAGGACCTCTTGAAGAGGCGACACACACACCCGTCAGTCAACC

111 111 111 111 111 111 111

CCNNCTCNNGAANCNANACGTCGCGGTGNNANNACGCTGTGGNNNGCGTCTGCNCGCGTTCCTT

440 450 460 470 480 490 500

900 910 920 930 940 950 960 970

GTTCGCCAGCAGACCCCGACCGAAACGAGGCAAGATTCCTCCCGGCTAGGCACTCGGAAGCAATGCTGAT

111 111 111 111 111 111 111 111

CCNNCNCCTTCCACCATCTTCTTACNGGCTCTCCNCGCTCTCNNNACNCCCTGGGAGCTTTCCTNTG

510 520 530 540 550 560 570 580

980 990 1000 1010 1020 1030 1040

GCTCCGATGGTGCAGCTCGGACAGG-GATTCGTCGAACCTTGATGAGCATGAGTGTCTTAGCGAGCAAGG

111 111 111 111 111 111 111 111

CCCCCTTNACTCCGCCCTTCGNGTGNCCCGNCCCGACCTCATTTNCANACGTCCTTCACAANNCCGTCG

590 600 610 620 630 640 650

1050 1060 1070 1080 1090 1100 1110

GTCTGTGCTACTCTGGTGGCTACGGAGAGGCTGGCGCTCCACCTCTGGCTCCCTGGCTCTGTGTCGGCT

111 111 111 111 111 111 111 111

GNTNNCTCCCNANCNGTNCNCAGGAAAGGNGGNGNCCNNTGTTGAC-GTTGNGNGANGTCC

660 670 680 690 700 710 720

1120 1130 1140 1150 1160 1170 1180

CAAGACTGTGAGGCCCGACCGCATGTGTAGGAGTTCTGGAACAGATGTGCGGCTGACAGCACCCCATCTGC

111 111 111 111 111 111 111 111

GAAANTCCTCNCCTCANCNCTACCCCTCGGGCGNNCTCTCNGTTNCCAACTTANCAANTCTCCCCCGNGN

730 740 750 760 770 780 790

1190 1200 1210 1220 1230 1240 1250

GATGCACGAGGACCGCCGAGCAGAACAAATTCGTTTCCATGACCACTGCCGCTGCCAGGCTGCGAGTGGCG

111 111 111 111 111 111 111 111

GCNCTCTCAGCCTCNCCCGNCCNCTCTCTGCACTGTCTGCTCTNACCNNTAGCATNTTCNCCNCC

800 810 820 830 840 850 860

1260 X

GGCTGCC

111

111

TCCTTCC

870 X

55. US-09-030-606-173' (1-1265)

US-09-020-747-10	Sequence 106, Application US09020747	
Initial Score	= 45	Optimized Score = 149
Residue Identity	= 35%	Matches = 170
Conservative Substitutions	= 12	Mismatches = 294
Gaps	= 0	Conservative Substitutions = 0
		Significance = 1.11

X 10 20 30 40 50 60
TTTTTTTTTGCNCNTCTTTAACTTTTCTGGACTCTAGGGAAGGACNNAATGAAAAAC---

ATGTTCCGGCCCACTCCCTCCNTCCNAANAAGTAATTCACCCGCCCCNCCNTCTNTTGCCTGGCCCTTAA	430	440	450	460	470	480	490
370	380	390	400	410	420	430	440
GGAGGGCTGGGGATCTGTACCCCTTGGTTTGGAGGAGGAGGGGCTGGGGCCCTGGACTCTCTGGCGCTGAGGG							
NTACCCACACGGGAACACTANTTATTCATCTTNGTGGCTGTNTATCNCNCCTGAAAGCGCCAAAG	500	510	520	530	540	550	560
450	460	470	480	490	500	510	
AGGAGGGCTGGGAACAGATATTCCTGAATTCCTCCGAGGAGTATTTGGGGGTCAATTCATGGGTTC							
TTGAAGGCCACGCGCTNCCNCCTCCCATAGNANNTTTTNNCNTCANCTAATATGCCCCGCCGGAACATC	570	580	590	600	610	620	630
520	530	540	550	560	570	580	
CAGTCCCGCAGAGTTAACTGGCTGGAGGGTTTCTCTATCCACTCAGTGAATTCGACAGGTTGGTGTAGAC							
CAATCCCCCCTT - GGGGGCCCGCAGCCCGCCCGCTCGGGNNCNCNCNAGTCCCGGAGTCC	640	650	660	670	680	690	700
590	600	610	620	630	640	650	
ACCTGGCAGCCCAACTTGGCCACACGGGGCTTTTCCGAAAGACACAGGCCCTGCAAGTACCGCTGCAGAT							
TCCCATCNGNCCNNGNCNCCCGGCACGACGACAANAAGGNTGAGCCNCCGCAANNNNNNNGTTNCCAC	710	720	730	740	750	760	770
780	790	800	810	820	830	840	
660	670	680	690	700	710	720	
CAGGGGCCCCCAGAGTACCGGTTGCAGGAGTCTCTTCTGGTCTTGCCTCCGCCGCGCAGAACATGCT							
CTCGCCCGCCCGCCNCGNG	790	800	810	820	830	840	

63. US-09-030-606-173' (1-1265)
US-09-020-747-31 Sequence 31, Application US/09020747

Initial Score	=	44	Optimized Score	=	190	Significance	=	1.04
Residue Identity	=	30%	Matches	=	213	Mismatches	=	457
Gaps	=		Conservative Substitutions	=	19		=	0

[illegible][illegible]

64. US-09-030-606-173' (1-1265)
US-08-806-596-8 Sequence 8, Application US/08806596

Initial Score	=	42	Optimized Score	=	253	Significance	=	0.90
Residue Identity	=	35%	Matches	=	305	Mismatches	=	492
Gaps	=		Conservative Substitutions	=	53		=	0

[illegible]

[illegible]

65. US-09-030-606-173' (1-1265)

US-08-086-596-27 Sequence 27, Application US/08806596

Initial Score	=	42	Optimized Score	=	234	Significance	=	0.90
Residue Identity	=	31%	Matches	=	266	Mismatches	=	551
Gaps	=	23	Conservative Substitutions	=			=	0

100
 CACANGGGGCACACTGTGTCNAGGGGAAATCTAGGTGGCATTTGGACCNCCTGGGTCTGANGGAAGAGGGGCTGG
 110
 120
 130
 140
 X
 150
 160
 TCTGGGTGATGGCCCTCTTCCTC
 X
 10
 20

GACTTNNACCTCTGGGTCAGGGAGCGGGTTGGGCGTTGGACCTCTGACTCTGAAGAGAGAGGGGTTC
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
CTCAGGACCTCTGACTGCTCTGGGCCAAGAATCTCTGTTCCTCCAGCCCCCAGCAGCGGGTGATTC

GGGGCCCAACCCCTGGGCTGTAGGGAGGAGGGGCTGGGGGGTCTGGACTCCTGGGCTGTGANGAGGAGGGG

[illegible]

66. US-09-030-606-173' (1-1265)

86. US-09-030-808-173 {1-1263}
US-08-904-809-27 Sequence 27, Application US/08904809

Initial Score	-	42	Optimized Score	-	227	Significance	-	0.90
Residue Identity	-	33%	Matches	-	286	Mismatches	-	531

170 180 190 200 210 220 230
TATGCTGGCCACTTCTTGAACAGGAGGTGGAGAGCCAGCATGGAACAAAGCTGCCAC--TTTCTAAAGT
730 740 750 760 770 780 790
TGCTGGGTGTACAGCGGTATAGAGTCTACTGCAGACCTCTCTCAGACACACCGACGACCTTACGCACT
ACCGAGACTTGCCCTGGCCCTGTGCACACTACTGATGACCTTCTGTGCTCGCAGATGGAATGTAGGGGTG
240 250 260 270 280 290 300
800 810 X 820 830 840 850 860
GCAGCAGGTAGGCATTCTGCCTGGACCGCAGAGCTCTGGGTACGCCCCCGGACTGGGCAGAGCACT
AGCTGTGACTCTATGGT
310 320 X

69. US-09-030-606-173' (1-1265)

US-08-904-809-8 Sequence 8, Application US/08904809

Initial Score = 41 Optimized Score = 253 Significance = 0.83
Residue Identity = 35% Matches = 305 Mismatches = 492
Gaps = 53 Conservative Substitutions = 0

50 60 70 80 90 X 100 110
GGAAAGGGACNAAATGAAACCAACTGTTAGGTGGGTCAACNTNCCACAAGGGGCACTGTGTNCAG
120 130 140 150 160 170 180
GGAAATCTAGTGGCATTTGACCCNCTGGGTCTGANGAAGAGGGGCTGGGACCTNNAACCTCTGGGTCTGGG
190 200 210 220 230 240 250
GAAAGGGGTTGGGGCTTGACCTCTGACCTCTGAAGGAGGAGGGGTTGGGGCTCAACCCCTGGGTCTGTG
260 270 280 290 300 310 320 330
AGGGAGGGGCTGGGGGTCTGGACTCTGGGTCTGANGGAGGAGGGGCTGGACTCTCTGGGTCTGAGGGA
AAACAGCTG-----GGACATATCCGCGAGTACGACAGCGCTGAA-----AGTGTGGAGCG
160 170 180 190 200
340 350 360 370 380 390 400
GGAGGGCTGGGGGTCTGGACTCTGGGTCTGAGGAGGAGGGGCTGGGATCTGTACCTTGGTTTGG
GGAGTCCACAGAGTGTAGCGCGTCTGGGTGGGTGGCGGAGGCGCTGACGCTCTGCC--TTGCTGCCCC
210 220 230 240 250 260 270
410 420 430 440 450 460 470
GAGGAGGGCTGGGGCTGGACTCTGGGCTGAGGGAGGAGGGGCTGGGAACAGATATTCCTGAATTCCT
CANGTGGGCGCCACCCCTGACCTGCCTGGGTCCAAACACTGAGCCCTGCTGGCGGACTTCAAGAGANAAC
280 290 300 310 320 330 340 350
480 490 500 510 520 530 540
TCCGAGGATGTATTGGGGGTCAATTTATGAGTTCAGTCCAGTCCCGAGAGTTAACTGGCGCTGGAGGGTTTC
CCACANGGGGATTTGTCCTANANT---AAGGCTCATCTGGGCTCGGCCCCCGCCACTGTGGGCTTG
360 370 380 390 400 410 420
550 560 570 580 590 600 610
TCTATCCACTCAGTGAATTTGAGAGGTTGGTGTAGACACTTGGACGCGCACTTGGCCACAGGGGCTTTT
TCTTTGANGTGAG-----CCCCATGCTCCTGGGCACTGTCTGNGGACCACTTTNGGAGTGTCTCCT
430 440 450 460 470 480
620 630 640 650 660 670 680
GCCCAGCCGATGGTGTAGGAGTTCTGGAAACAGT---GTGCGGCTGACAGACCCACTTCCGATGCAACCAG
1130 1140 1150 1160 1170 1180 1190
GCCCAGCCGATGGTGTAGGAGTTCTGGAAACAGT---GTGCGGCTGACAGACCCACTTCCGATGCAACCAG

CCGAAGACACAAAGGCCCTGCAAGTACCCTTGCAGATCAGGGGGCCCCCAGAGTCA--CCGTTGAGAGGT
770 780 790 800 810 820 830
CCTCTGTGCTTTGGCCCTCCCGCGGCGCAGAACATGCTGGGGTGTACAGCGGTCAATAGAGCTTACTTCGAGA
NNTNCTANAACCGCGCCNCCCGCTGGAACCCNC-----CTTNTGTCTCTTTTNTNAGGCTTA
560 570 580 590 600 610
690 700 710 720 730 740 750 760
CCTCTGTGCTTTGGCCCTCCCGCGGCGCAGAACATGCTGGGGTGTACAGCGGTCAATAGAGCTTACTTCGAGA
ATNNGCCTTGGCCTTNCANNNGTCTCTNCNNTTTTCCNNTGTNAATTTTANGCNCNCCNNTCCNC
620 630 640 650 660 670 680 690
840 850 860 870 880 890 900
GGTACGCCCCCGGACTGGGCAGAGACCTCTTGAAGAGGCGACACACACACCGGTGAGCTACCGTTCCG
NNCNNCNCCCGACCCNANNNTNANNNCCTGGGGTNCNCCNNGATTGACCCNCCNCCCTNANTTGC
700 710 720 730 740 750 760
910 920 930 940 950 960 970
CAGCAGACCCCGCAGAAACGAGAGTTCGCCGCGGTAGGCACTGCGAAGCAATGCTGATGCTCCG
NTTNGGNNCNTGCCCCCTTCCCTCTNGGANNCG
770 780 790 X
980 990
GATGCTGTGAGACT

70. US-09-030-606-173' (1-1265)

US-09-020-747-90 Sequence 90, Application US/09020747

Initial Score = 40 Optimized Score = 122 Significance = 0.76
Residue Identity = 33% Matches = 142 Mismatches = 255
Gaps = 24 Conservative Substitutions = 0

770 780 790 800 810 820 830
CAGACACCACGACAGCTTTCAGCAGCTGACGACGCTAGGCACTTTCGCTGGCAGCAGAGCTCTGGGTGAG
840 850 860 870 880 890 900 910
CCCCGCGACTGGGAGAGGACCTCTTGAAGAGGCGCAGACACACACCGGTGAGCTCACCGTTCGCCAGCAG
TGTCGAGCTGTTTCANCCACCAACTCTACAAGTGTCTTCCACTCACTGTCTGTAAGCTNTNTAAACCAG
30 40 50 60 70 80 90
920 930 940 950 960 970 980
ACCCAGCCAGAAACGAGGCAAGAGTTCGCCGCGGTAGGCGACTGCGAAGCAATGCTGATGCTCCGGATGGT
ACTGATCTTCATAATAAGAAATTTCTCACAGTCACTCTCTAGGACCTTTTGGATTCAGTTAGTA
100 110 120 130 140 150 160
990 1000 1010 1020 1030 1040 1050
GTCAGACTCGGACGAGTTCCTCAACTTGTGATGAGCATGAGTCTGTAGCAGCAAGGCTCTGTGTACTC
TAAGTCTTCCACTTCTTGTGTAAGACTTCAT-----CTGGTAAAGTCTTAAGTTTG
170 180 190 200 210 220
1060 1070 1080 1090 1100 1110 1120
TGGGTCGCTACGAGAGGCTGGCTCCACATCTGGCTCTGGCTTGGTGGCCTCAGAGCTGCGAG
TAGAAGGAATTAATTTGCTGCTTCTTAACAACTGCTCTCTCTTGAAGTATTGGCTGAGAAC--CCAC
230 240 250 260 270 280
1130 1140 1150 1160 1170 1180 1190
GCCCAGCCGATGGTGTAGGAGTTCTGGAAACAGT---GTGCGGCTGACAGACCCACTTCCGATGCAACCAG
1130 1140 1150 1160 1170 1180 1190
GCCCAGCCGATGGTGTAGGAGTTCTGGAAACAGT---GTGCGGCTGACAGACCCACTTCCGATGCAACCAG

CTNAAGTCCCTTTGTGCATCCATTTTAAATATACTTAATAGGGCATTTGGTNCACCTAGGTAAATTCGCAAG
290 300 310 320 330 340 350 360
1200 1210 1220 1230 X 1240 1250 1260
GAGCCCGGACGAGAACAAATTCGTTTTCATGACCAAGTCCCGCTGCCAGGGCTGCGAGTGGCGGCTGCC
AGTCATCTGTCTGCAAAAGTTGCGTTAGTATATCTGCCA
370 380 390 400


```
240 250 260 270 280 290 300 310
TACCGGGGAACCTTTCCTTCGCTTCGGCTGGGCTGCTGGGGAACGGTGAGCTCACGGGTGTGTCTT
|||||
TACCGGGGAACCTTTCCTTCGCTTCGGCTGGGCTGCTGGGGAACGGTGAGCTCACGGGTGTGTCTT
320 330 340 350 360 370 380
GCCCTTCATAGGAGGTCCTCTGCCAGTCGCGGGGCTGACCCAGAGCTTGGCTCCAGGCAGAAATGCCT
|||||
GCCCTTCATAGGAGGTCCTCTGCCAGTCGCGGGGCTGACCCAGAGCTTGGCTCCAGGCAGAAATGCCT
390 400 410 420 430 440 450 460
320 330 340 350 360 370 380
GCCCTTCATAGGAGGTCCTCTGCCAGTCGCGGGGCTGACCCAGAGCTTGGCTCCAGGCAGAAATGCCT
|||||
GCCCTTCATAGGAGGTCCTCTGCCAGTCGCGGGGCTGACCCAGAGCTTGGCTCCAGGCAGAAATGCCT
470 480 490 500 510 520 530
330 340 350 360 370 380 390
ACCGTGTGCAAGTGCCTGCAAGCTGTCGGTGTGCTGANGAGGCTGCAANTAGCTCTATGACCGGTGTAC
|||||
ACCGTGTGCAAGTGCCTGCAAGCTGTCGGTGTGCTGAGAGGCTGTCAGTAAGCTCTATGACCGGTGTAC
440 450 460 470 480 490 500 510 520 530
460 470 480 490 500 510 520
CACCCANCATGTTCTGGCGCGGGGGAAGACACAGAGGAGTCTGCAAGCTGAGAGGGGAAGG
|||||
CACCCANCATGTTCTGGCGCGGGGGAAGACACAGAGGAGTCTGCAAGCTGAGAGGGGGG
540 550 560 570 580 590 600
530 540 550 560 570 580 590
GAGGCGAGGCGCACTCAGGGAAGGTTGGAGAGGGGACAGACAGACAGAGCGCGCATGGCGAGATGCAG
|||||
CCTGATCTGCAACCGGTACTTGCAGGGCTTGTGCTTTCGGAAGAGCGGCTGGCCAAAGTTGGCGTGCC
610 620 630 640 650 660 670
600 610 620 630 640 650 660 670
AGATGGAGAGACACAGAGGAGACAGTGCACAACTAGAGAGAGAACTGAGAGAAACAGAGAAATAACACAG
|||||
AGGTGCTTACAC-----CAACCTCTGCAAAATTCAGTGTGATAGAGAAACCCCTCCAGGCCAGTTAA
680 690 700 710 720 730 740
680 690 700 710 720 730 740
GAATTAAGAGAGCAAGAGAGAGAGAAACAGACATGGGAGGCGAGAAACACACACACATAGAAAT
|||||
CTCTGGGACCTGGGAACCCATGAAATGACCCCAATACATCTCGGGAAGGAATTCAGGAATATGTGTC
750 760 770 780 790 800 810
750 760 770 780 790 800
GCAGTTGACCTTCCACAGATGGGCTGAGGGGGGA-----CCTCACCCATAGAAATCCT
|||||
CCAGCCCTCTCCTCCTCAGGCCAGAGGTCCAGGCCCCAGCCCTCCTCCTCAAAACCAAGGATACAGATC
820 830 840 850 860 870 880
810 820 830 840 850 860 870
CTTATTAAGTCTTCTCCCAAAACCTGACTAGAAATAGCTTACTGTTGAGGGGAGCCCTTACCAATAACA
|||||
CCAGCCCTCTCCTCCTCAGACCCAGAGGTCCAGACCCCGCCCTCCTCCTCAGACCCAGAGGTCCAG
890 900 910 920 930 940 950
880 890 900 910 920 930 940
TAATATAGTCGATTTATGATAGCTTTTATGCAATCATGATATACCTTTGTTGGAAATTTTGTATATTTCTAA
|||||
CCCTCTCTCTCCTCAGACCCAGAGGTCCAGACCCCGCCCTCCTCCTCAGACCCAGGGGTTGAGGCCCC
960 970 980 990 1000 1010 1020
950 960 970 980 990 1000 1010 1020
GCTACAGAGTCTGCTGTGAATTTTAAATTTGTTGCAACTCTCCTAATAATTTTCTGTGTGTATTGTA
|||||
CAACCCCTCTCTCCTCAGAGGTCCAGACCCCAAGCCCGCCCTGTTCCCGACCCAGAGGTNNAGGTC
1030 1040 1050 1060 1070 1080 1090 1100
1030 1040 1050 1060 1070 1080 1090 1100
AAAATCCCAAGTATAGTGGACTTGTGCAATTAACACAGGGTGTGTTCAAGGGTCAACTGTGTACCCAGAGG
|||||
CCAGCCCTCTCTCCTCAGACCCAGAGGTCCAGACCCCAAGCCCGCCCTGTTCCCGACCCAGAGGTNNAGGTC
1110 1120 1130 1140 1150 1160 1170
1100 1110 1120 1130 1140 1150 1160 1170
1100 1110 1120 1130 1140 1150 1160 1170
```

```
AAACAGTCACACAGATTCATAGAGGTGAACACGAGAACAGAGAAATCAAGACTCTACAAAGAGGCT
|||||
GNANGTTGACCCACACCTTACAGTTGGTTTTTTCATTTTNGTCCCTTTCCCTAGATCCAGAAATAAAGTTT
1180 1190 1200 1210 1220 1230 1240
1170 1180 1190 1200 1210 1220 1230
GGGAGAGGTGGCTCATGCTCTAATCCAGCAGCTTTGGGAGGAGGAGGAGATCATCTTGAGGTAAAGGA
|||||
AAGAGANGNGCAAAAAA
1250 1260 X
Initial Score = 482 Optimized Score = 597 Significance = 6.16
Residue Identity = 53% Matches = 674 Mismatches = 454
Gaps = 127 Conservative Substitutions = 0
```

3. US-09-030-606-174 (1-1459)
US-09-020-747-17 Sequence 171, Application US/09020747

```
GGAAAAAGAAATTTCTGCTCGGGCGTCTCTGCTGTCATCCGAGTGGGTGCTGTGACGCGCACACTGTTTCCA
70 80 90 100 110 120 130 140
30 40 50 60 70 80 90
GAAAGTGTGAGAGTCTCTACACCATCGGCTGGGCTGCACAGTCTTGAGGCGGACCAAGAGCCAGGAG
|||||
GAAAGTGTGAGAGTCTCTACACCATCGGCTGGGCTGCACAGTCTTGAGGCGGACCAAGAGCCAGGAG
150 160 170 180 190 200 210
100 110 120 130 140 150 160
CCAGATGTGGAGGCGGCTCTCCGTACGCGCACCCAGAGTACACAGACCTTGTCTCGCTAAGACCTCAT
|||||
CCAGATGTGGAGGCGGCTCTCCGTACGCGCACCCAGAGTACACAGACCTTGTCTCGCTAAGACCTCAT
220 230 240 250 260 270 280
170 180 190 200 210 220 230
GCTCATCAAGTTGAGAGCAATCCGTGTCGAGTCTGACACCATCCGAGCATCAGCATTTGCTTCGAGTGCCC
|||||
GCTCATCAAGTTGAGAGCAATCCGTGTCGAGTCTGACACCATCCGAGCATCAGCATTTGCTTCGAGTGCCC
290 300 310 320 330 340 350
240 250 260 270 280 290 300 310
TACCGCGGGAACCTTTCGCTCGTTTCTGGCTGGGCTGCTGGCGAACGCTGAGCTCACGGGTGTGTCT
|||||
TACCGCGGGAACCTTTCGCTCGTTTCTGGCTGGGCTGCTGGCGAACGCTGAGCTCACGGGTGTGTCT
360 370 380 390 400
320 330 340 350 360 370 380
GCCCTCTTCAAGAGAGTCTCTGCGGCGGCTGACCCAGAGCTTGTGCTCCAGGAGAGTGCCT
|||||
-----GGCAGAAATGCCT
410
390 400 410 420 430 440 450
ACCGTGTGAGTGGTGAACCTGTCGGTGTGCTGANGAGGTGTCGANTAGCTCTATGACCGGTGTAC
|||||
ACCGTGTGAGTGGTGAACCTGTCGGTGTGCTGANGAGGTGTCGANTAGCTCTATGACCGGTGTAC
420 430 440 450 460 470 480
460 470 480 490 500 510 520
CACCCANCATGTTCTGGCGCGGGGGAAGACCAAGAGGACTCTGCAAGCTGAGAGGGGAAGG
|||||
CACCCANCATGTTCTGGCGCGGGGGAAGACCAAGAGGACTCTGCAAGCTGAGAGGGG
490 500 510 520 530 540 550 560
530 540 550 560 570 580 590
GAGGCGAGGCGCACTCAGGGAAGGTTGGAGAGGGGAGACAGACACAGAGCGCGCATGGCGAGATGCAG
|||||
CCTGATCTGCAACCGGTACTTGTGCTTTCGGAAGAGCGGCTGGCCAAAGTTGGCGTGCC
570 580 590 600 610 620 630
```


[illegible]

US-09-030-606-174 (1-1459)	US-09-020-747-17 Sequence 175, Application US/09020747
Initial Score =	442
Optimized Score =	563
Significance =	5.61
Residue Identity =	52%
Matches =	644
Mismatches =	442
Conservative Substitutions =	139
Non-conservative Substitutions =	0

GGAAACGAATTGTTCTGCTCGGCGCTCTGTGTCATCCGACATGGGTGCTGTGCACGCCGCACACTGTTTCCA
X
GGTCAGCCGCACACACTGTTTCCA

30 40 50 60 70 80 90
GAAGTCAGTGCAGAGCTCCTTACACATCTGGGCTGGCGCTGCACAGTCTTAGGCGACCAAGCAGCGAGGAG
GAA-----CTCTACACCATCGGCTGGCGCTGCACAGTCTTAGGCGCACCAAGAGCAGCGAGGAG
110 120 130 140 150 160
100 110 120 130 140 150 160
CCAGATGGTGGAGCGAGCCTTCGGTACGCGACCCAGAGTACACAGACGCTTGTCTCCTAACGACCTCAT
CCAGATGGTGGAGCGAGCCTTCGGTACGCGACCCAGAGTACACAGACCTTGTCTCCTAACGACCTCAT
170 180 190 200 210 220 230
GCTCATCAAGTTGGAGCGAATCCGTTCCGAGTCTGCACACCATCGGAGCATCAGCATTTGCTTCGACAGTGCCT
GCTCATCAAGTTGGAGCGAATCCGTTCCGAGTCTGCACACCATCGGAGCATCAGCATTTGCTTCGACAGTGCCT
240 250 260 270 280 290 300
170 250 260 270 280 290 300
TACCGGGGGAACCTTTCGCTTCGTTTCGGTGGGCTCTGCTGGCGAACGGTGAAGCTTCACGGTGTGTGTCT
TACCGGGGGAACCTTTCGCTTCGTTTCGGTGGGCTCTGCTGGCGAACGGTGAAGCTTCACGGTGTGTGTCT
310 320 330 340 350 360 370 380
TACCGGGGGAACCTTTCGCTTCGTTTCGGTGGGCTCTGCTGGCGAACGGTGAAGCTTCACGGTGTGTGTCT
GCCCTCTTCAAGAGGTCCTCTGCCAGTCGCGGGGCTGACCCAGAGCTCTGCTCCAGGCGAGATGCGCT
390 400 410 420 430 440 450
ACCCTGTGTCAGTGCCTGTAACGTTGTCGGTGTCTGANGAGGTCTGCANTAACTCTATGACCCGCTGTAC
ACCCTGTGTCAGTGCCTGTAACGTTGTCGGTGTCTGANGAGGTCTGCANTAACTCTATGACCCGCTGTAC
370 380 390 400 410 420 430
460 470 480 490 500 510 520
CACCCCAACATGTTCTCGCGCGCGGAGGCGACAGACCAAGAGACTCTCTCAACCTGAGAGGGGGAAGGG
CACCCCAACATGTTCTCGCGCGCGGAGGCGACAGACCAAGAGACTCTCTCAACCTGAGAGGGGGAAGGG
440 450 460 470 480 490 500
CAGCCGAGCATGTTCTCGCGCGCGGAGGCGACAGACCAAGAGACTCTCTGCAAC-----GGTGACTCT
530 540 550 560 570 580 590
GAGGCGAGCGCACTCAGGAGAGGTTGAGAGGAGGAGACAGACACAGGGCGCATGGCGAGTGCAG
GAGGCGAGCGCACTCAGGAGAGGTTGAGAGGAGGAGACAGACACAGGGCGCATGGCGAGTGCAG
600 610 620 630 640 650 660 670
AGATGAGAGACACACAGGGAGACGTGCACTAGAGAGAGAACTGAGAGAAACAGAGAAATAACACAGAG
AGATGAGAGACACACAGGGAGACGTGCACTAGAGAGAGAACTGAGAGAAACAGAGAAATAACACAGAG
680 690 700 710 720 730 740
GAATAAGAGAGACAAAGAGAGAGAGAAACAGAAACAGATGGAGAAACAGAGAAATAACACAGAG
GAATAAGAGAGACAAAGAGAGAGAGAGAAACAGAAACAGATGGAGAAACAGAGAAATAACACAGAG
750 760 770 780 790 800 810
CTCTGGGACTGGGAAACCCATGAATTCACCCCAATACATCTCTCGGAAGAAATTCAGGAATATCTGTT
CTCTGGGACTGGGAAACCCATGAATTCACCCCAATACATCTCTCGGAAGAAATTCAGGAATATCTGTT
820 830 840 850 860 870 880
GCAATTGACCTTCCACAGACATGGGCGCTGAGGGCGGTGACCTCCACCCCAATAGAATTCCTTATACTT
GCAATTGACCTTCCACAGACATGGGCGCTGAGGGCGGTGACCTCCACCCCAATAGAATTCCTTATACTT
890 900 910 920 930 940 950
CCAGCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCAGCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
960 970 980 990 1000
TTGACTTCCCCAAAACCTGACTAGAAAATAGCCTACTGTTGAGGGGAGCCTTACCATACATATAATGCTG
TTGACTTCCCCAAAACCTGACTAGAAAATAGCCTACTGTTGAGGGGAGCCTTACCATACATATAATGCTG
1010 1020 1030 1040 1050 1060 1070
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
1080 1090 1100 1110 1120 1130 1140
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
1150 1160 1170 1180 1190 1200 1210
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
1220 1230 1240 1250 1260 1270 1280
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
1290 1300 1310 1320 1330 1340 1350
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
1360 1370 1380 1390 1400 1410 1420
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
1430 1440 1450 1460 1470 1480 1490
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
1500 1510 1520 1530 1540 1550 1560
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
1570 1580 1590 1600 1610 1620 1630
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
1640 1650 1660 1670 1680 1690 1700
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
1710 1720 1730 1740 1750 1760 1770
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
1780 1790 1800 1810 1820 1830 1840
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
1850 1860 1870 1880 1890 1900 1910
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
1920 1930 1940 1950 1960 1970 1980
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
1990 2000 2010 2020 2030 2040 2050
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
2060 2070 2080 2090 2100 2110 2120
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
2130 2140 2150 2160 2170 2180 2190
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
2200 2210 2220 2230 2240 2250 2260
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
2270 2280 2290 2300 2310 2320 2330
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
2340 2350 2360 2370 2380 2390 2400
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
2410 2420 2430 2440 2450 2460 2470
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
2480 2490 2500 2510 2520 2530 2540
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
CCCA-GCCCTCTCTCCCTCAGGCCCCAGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGATACAGAT
2550 2560 2570 2580 2590 2600 2610
CCCA-GCCCTCTCTCCCTCAGGCCCCAG

AGAATGCCTACCGTGCAGTGCCTGAACGTGTCGGTGTCTGAGNGGCTCGCAGTAAGCTCTATGAC
190 200 210 220

[illegible]

160 170 180 190 200 210 220
CGACCTCATGCTCATCAAGTTGGACGAATCCGTTCCGAGTCTGACACATCCGAGCATCAGCATTTGCTTC
CGACCTCATGCTCATCAAGTTGGACGAATCCGTTCCGAGTCTGACACATCCGAGCATCAGCATTTGCTTC
CGACCTCATGCTCATCAAGTTGGACGAATCCGTTCCGAGTCTGACACATCCGAGCATCAGCATTTGCTTC
230 240 250 260 270 280 290 300
GCAGTGCCTTACCGGGGGAACTCTTGCTGTTTGGCTGGGGTCTGCTGGCAAGCGTGAGCTCACGGG
GCAGTGCCTTACCGGGGGAACTCTTGCTGTTTGGCTGGGGTCTGCTGGCAAC-----
GCAGTGCCTTACCGGGGGAACTCTTGCTGTTTGGCTGGGGTCTGCTGGCAAC-----
100 110 120 130 140 150

310 320 330 340 350 360 370
TGTTGTCTGCCCTCTTCAGGAGGTCCTCTGCCAGTCGGGGGGGTGACCCAGAGCTCTGGCTCCACGGC
|||-----GGC

[illegible]

7. US-09-030-606-174 (1-1459) Application US/09020747

Initial Score	=	154	Optimized Score	=	200	Significance	=	1.65
Residue Identity	=	73%	Matches	=	232	Mismatches	=	2
Gaps	=		Conservative Substitutions	=	83		=	0

90 100 110 120 130 140 150
 GCCAGGAGCCAGATGTTGGAGCCAGCCTTCCTAGCGACCCAGATACACAGAGACCTTCTCGCTAA
 y acaacagaccccttgcctcgcttaa 20

160 170 180 190 200 210 220
CGACCTCATGCTCATCAAGTTGACGAATCCGCTGCCAGTCTGACACCATCCGGAGCATCAGCATTCCTTC
CGACCTCATGCTCATCAAGTTGACGAATCCGCTGCCAGTCTGACACCATCCGGAGCATCAGCATTCCTTC
CGACCTCATGCTCATCAAGTTGACGAATCCGCTGCCAGTCTGACACCATCCGGAGCATCAGCATTCCTTC

[illegible]

380 389 390 400 410 420 430 440
AGATGCCTACCGTGTCCAGTGCCTGAACGTGTCGGTGGTGTCTCGANGAGCTCTGCANTAAAGCTCTATGAC

8. US-09-030-606-174 (1-1459)

US-09-030-606-174 (1-1459)
US-08-904-809-26 sequence 26, Application US/08904809

Initial Score	=	77	Optimized Score	=	218	Significance	=	0.59
Residue Identity	=	30%	Matches	=	249	Mismatches	=	560
Gaps	=		Conservative Substitutions	=	15		=	0

AGATCCAGAGATGGAGAGACACACAGGGAGACGTGCAACTACAGAGAGAACTGAGAGAAACAGAGAAAT
600 610 620 630 640 650 660
ANATTANTACAGTGTATCTTT
y 10 20

AAACACAGGAATTAAGAGAAGCAAAAGGAGAGAGAGAAACAGAACAGACATGGGAGGCAGAAACACACACAC
730

DNA sequence

740 750 760 770 780 790 800
ATAGAATGCAGTTGACCTTCCAACAGCATGGCGCCTCAGGCCGTGACTCCACCCTAATAAGAAATCCTCT
||| ||| |
CAAGAGTGCTGGGTCATTCTCGAANAAGTGGCGGCCCCCACCTCCTCTCTCCCATAGCCATCC
150 160

[illegible]

880
AATAGTCGATTATGCATACGTTTATGCATTCATGATATACCTTTGTTGGAAATTTTGTATATCTTAAAGC
950

240 250 260 270 280 290 300

TACACAGTCTGTCGAATTTTTTAATTTGTGCAACTCTCAAATTTTCTGATGTGTTATTGAAA
||||| ||| ||| ||| ||| ||| ||| ||| |||
GTCACACTATAAAGTTAAACGAGCNAGAYNANACGGCTTCAGTGCCACCTTCCTCTACTGACNACCAGNG

310 320 330 340 350 360 370 380 390

[illegible][illegible]

1170 1180 1190 1200 1210 1220 1230
 TGGCAGGGTGGCTCATGCGTGTAAATCCAGCACATTTGGGAGCGGAGGCAGCATCTTGAGTGAAGGA

1240 1250 1260 1270 1280 1290 1300
GTTCAAGACGAGCCTGGCCAAATGGTGAATCCTGCTGTACTAAAAATACAAAGTTAGCTGGATATGGT

[illegible]


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TTTTGATATTTCTAAGCTACACAGTTCGCTGTGAATTTTTTAAATTTGTGCAACTCTCCTAAATTTT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TTTTTCCCTTTTCTGTAGCGCGCTTAAGCTTTCTAAATTTTGAACATCTAAGCAAGCTGAANGAAAGGG
170 180 190 200 210 220 230

1010 1020 1030 1040 1050 1060 1070
CTGATGTTTATGAAAAATCCAGTATAGTGAGCTTGTGCATTCAAACC-AGGTTTGTTCAGGGTCA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GGTTTCGCAAAATCACTCGGGGAANGAAGGTTGCTTTGTTAATCATGCGCTATGTTGGTGTATTAACGT
240 250 260 270 280 290 300

1080 1090 1100 1110 1120 1130 1140
ACTGTGTACCCAGAGGGAACAGTGACACAGATTCATAGAGTGAACACAGAGAACAAGAAATCAAA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CTTGTACAAATTTACNTTTCACCTTTTAAATTAATTTGCTNAANGCTTTAATTANACTTGGGGGTTCCCTCCCA
310 320 330 340 350 360 370

1150 1160 1170 1180 1190 1200 1210
GACTCTACAAAGAGGCTGGGAGGCTGCTCATGCTGTATCCAGC--ACTTTGGAGGGAGGAGGCA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
NACCAACCCCTGACAAAAAGTCCCGCCCTCAAAATNATGTCCCGCNCNTTGAACACACACNGCNGAAN
380 390 400 410 420 430 440 450

1220 1230 1240 1250 1260 1270 1280
GATCACTGAGTGAAGGTTCAAGACCCAGCTGGCCAAATGTGAATCTGTCTACTTAAATAACAA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GTTCTCATTTNTCCCNCCAGGTNAATTAAGGGTTTACCATNTTTAAACCCACCTCCACNTGGCNGGCC
460 470 480 490 500 510 520

1290 1300 1310 1320 1330 1340 1350 1360
AAGTTAGTGTATGTTGGAGCGGCTGTAAATCCAGCTACTTTGGAGGCTGAGGAGGAGATTTGCTTG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TGAATCTTCNAANCCCTCAANCNAATTTNCTNNGCCCGGTCNCGTCNNGTCCCGCCGCTCCGGG
530 540 550 560 570 580 590

1370 1380 1390 1400 1410 1420 1430
AATATGGGAGGAGGTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AANTNACCCCGCNGAANNCTNNTNACNAATTCGAAATATTCCTNNTCTCAATTCCTCCCNAGAC
600 610 620 630 640 650 660

1440 1450
TCTGTCTCAAAAAA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TNTCTCNANCNCAATTTCTTTTNTTCAGCAACNGCNGNCCNNAATGNNNNNCCTCCCTNGTCC
670 680 690 700 710 720 730

NNA
740

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13. US-09-030-606-174 (1-1459)

US-09-020-747-39 Sequence 39, Application US/09020747

Initial Score = 73 Optimized Score = 202 Significance = 0.54
 Residue Identity = 31% Matches = 217 Mismatches = 473
 Gaps = 6 Conservative Substitutions = 0

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AGGCAGAAACACACACATAGAAATGCAGTTGACCTTCCAAACAGCATGGGCGGTGACCTCCA
720 730 740 750 760 770 780
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TNTCTCNANCNCAATTTCTTTTNTTCAGCAACNGCNGNCCNNAATGNNNNNCCTCCCTNGTCC
670 680 690 700 710 720 730

NNA
740

790 800 810 820 830 840 850 860
CCCAATAGAAAATCCTTATTAACCTTTGACTCCCAAAAACCTGACTAGAAATAGCCTACTGTTGACGGG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CACATTTAATTTTATTTGATTTTATTAATGCTGCACAC---ACAATATTTATTCATTTGTTCTTTT
30 40 50 60 70 80 90

870 880 890 900 910 920 930
AGCCTTACCAATAACATAAGTAGTGATTTATGATACGTTTATGATCATTCATATACCTTCTTGAAT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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ATTTCATTTTATTTGTTGCTGCTGCTCTTTTATTTATTTTACTGAAAGTGAGAGGAACTTTTGTGGCCT
100 110 120 130 140 150 160

940 950 960 970 980 990 1000
TTTTTGATATTTCTAAGCTACACAGTTCGCTGTGAATTTTTTAAATTTGTGCAACTCTCCTAAATTTT
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TTTTTCCCTTTTCTGTAGCGCGCTTAAGCTTTCTAAATTTTGAACATCTAAGCAAGCTGAANGAAAGGG
170 180 190 200 210 220 230

1010 1020 1030 1040 1050 1060 1070
CTGATGTTTATGAAAAATCCAGTATAGTGAGCTTGTGCATTCAAACC-AGGTTTGTTCAGGGTCA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GGTTTCGCAAAATCACTCGGGGAANGAAGGTTGCTTTGTTAATCATGCGCTATGTTGGTGTATTAACGT
240 250 260 270 280 290 300

1080 1090 1100 1110 1120 1130 1140
ACTGTGTACCCAGAGGGAACAGTGACACAGATTCATAGAGTGAACACAGAGAACAAGAAATCAAA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
CTTGTACAAATTTACNTTTCACCTTTTAAATTAATTTGCTNAANGCTTTAATTANACTTGGGGGTTCCCTCCCA
310 320 330 340 350 360 370

1150 1160 1170 1180 1190 1200 1210
GACTCTACAAAGAGGCTGGGAGGCTGCTCATGCTGTATCCAGC--ACTTTGGAGGGAGGAGGCA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
NACCAACCCCTGACAAAAAGTCCCGCCCTCAAAATNATGTCCCGCNCNTTGAACACACACNGCNGAAN
380 390 400 410 420 430 440 450

1220 1230 1240 1250 1260 1270 1280
GATCACTGAGTGAAGGTTCAAGACCCAGCTGGCCAAATGTGAATCTGTCTACTTAAATAACAA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GTTCTCATTTNTCCCNCCAGGTNAATTAAGGGTTTACCATNTTTAAACCCACCTCCACNTGGCNGGCC
460 470 480 490 500 510 520

1290 1300 1310 1320 1330 1340 1350 1360
AAGTTAGTGTATGTTGGAGCGGCTGTAAATCCAGCTACTTTGGAGGCTGAGGAGGAGATTTGCTTG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TGAATCTTCNAANCCCTCAANCNAATTTNCTNNGCCCGGTCNCGTCNNGTCCCGCCGCTCCGGG
530 540 550 560 570 580 590

1370 1380 1390 1400 1410 1420 1430
AATATGGGAGGAGGTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
AANTNACCCCGCNGAANNCTNNTNACNAATTCGAAATATTCCTNNTCTCAATTCCTCCCNAGAC
600 610 620 630 640 650 660

1440 1450
TCTGTCTCAAAAAA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TNTCTCNANCNCAATTTCTTTTNTTCAGCAACNGCNGNCCNNAATGNNNNNCCTCCCTNGTCC
670 680 690 700 710 720 730

NNA
740

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14. US-09-030-606-174 (1-1459)

US-08-904-809-44 Sequence 44, Application US/08904809

Initial Score = 69 Optimized Score = 267 Significance = 0.48
 Residue Identity = 34% Matches = 300 Mismatches = 540
 Gaps = 21 Conservative Substitutions = 0

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GGGAGACAGACACACAGGGCGCGCATGGCGAGATGCAGAGATGGAGAGACACACAGGAGACAGTGA
560 570 580 590 600 610 620 630
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
ACATAATATCAGAGAAAGTA
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
X 10 20

640 650 660 670 680 690 700
CTAGAGAGAACTGAGAGAAACAGAGAAATAAACACAGAGGAATAAAGAGAGAGAGAGAGAACAG
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
GTCCTTGAATATTTACGTCACGAGGATTTCTTTGTTCTGATTATTATTTGGTGTGTTGTTGCCAA
30 40 50 60 70 80 90

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[illegible]

710 720 730 740 750 760 770
AAACAGACATGGGAGCGCAGAACAACACACATAGAAATGCGATTGACCTTCCACACGATGGGGCTGAG
GTATTGGCAGCTTCAGTTTTTCATTCTCTCATCTCCATCCCTGGGCATT---140 150 160
100 110 120 130 140 150 160
780 790 800 810 820 830 840
GGCGGTGACCTCCACCACATAGAAAATCTCTTATAACTTTTGACTC-----CCCAAAAACCTGACTAGAA
TTTCGTCCATCCACACGCTCCAGAATTTCTTTTGTGATAATATCTCATAGCTCGCTGAGCTTTTTCATAGG
170 180 190 200 210 220 230
850 860 870 880 890 900 910
ATAGCTACTGTTGACGGGAGCCTTACCAATAACATAAATAGTCGATTTTATGCATACCTTTTATGCAATCA
TCATGCTGCTGTTGTTCTCTTTTACCCCATAGCTGACCCACTGCCTCTGATTTCAGAAGCTCGAAGACGCG
240 250 260 270 280 290 300
920 930 940 950 960 970 980
TGATATACCTTTGTTGGAATTTTGTGATTTTCTAAGCTTACACAGTTGCTGCTGTAATTTTTTAAATTTGTT
CCTCAGATCGGTCTCCCACTTTTATTAATCCTCGGTTCTTGTCTGGTTCAGAAGAGATGTCGCGGATGAAT
310 320 330 340 350 360 370
990 1000 1010 1020 1030 1040 1050
GCAACTCTCTAAATTTTCTGATGTTTATTTGAAAAATCCCAAGTATAGTGGACTTG-TGCATTCAAA
CCCNATGAGTGAGTCCCTCTCGGTTGTGCTTTTGGTGTGGCACTGGCAGGGGGTCTTGCTCCCTTTTCA
380 390 400 410 420 430 440 450
1060 1070 1080 1090 1100 1110 1120
CCAGGGTGTGTTCAAGGGTCAACTGTGTACCAGAGGGAACAGTGCACAGATTACATAGAGTGTGAACACGA
TATCAGGTGACTCTGCAACAGGAAGTGACTGSGTGTTCATGGAGA-----TCTGAGCCCGCAGAAAGT
460 470 480 490 500 510
1130 1140 1150 1160 1170 1180 1190
AGAGAAACAGAAAAATCAAGACTCTCAAGAGGCTGGCAGGGTGGCTCATGCTGTAATCCGACACTT
TTTGCTGTCCAACAAATCTACTGTGCTACCATGATGGTGTGCATATAAATAGTCTTGCTTTTCCAGGTGTT
520 530 540 550 560 570 580
1200 1210 1220 1230 1240 1250 1260
TGGGAGGCGAG--CAGCGAGTCACTTCAGTAGAGGCTCAAGACGAGCTGGCCAAATGTGGAATCC
CATGATGAAGGCTCACTTTGTTGCTGTGACATGACATGTTGTGTGACTTGAACAGGTCACACTGCA
590 600 610 620 630 640 650 660
1270 1280 1290 1300 1310 1320 1330 1340
TGCTGTACTAAAAATACAAAAGTACGTGGATGTTGGGAGCGGCGCTGTATCCAGCTACTTTGGCAGGC
CTGGCGGTCCACTTCAGATGCTGCAAGTTGCTGTAGAGAGAGTGGCCCGCGCTGCTGCCCGCGGTGGA
670 680 690 700 710 720 730
1350 1360 1370 1380 1390 1400 1410
TGAGTCAGGAGAAATTCGTTGAA---TATGGGAGGAGAGGTTGAAGTCAGTTGAGATCACACCACCTATACT
CTCTCGCAAACTCATGCTGCAAAAGGTGCTCGCGGTTGATGTGCGAACTNTGGAAGGATACAAATGGCATC
740 750 760 770 780 790 800
1420 1430 1440 1450 X
CAGCTGGGCAACAGAGTATAGCTCTGCTCTCAAAAAAATAAAAAA
|||||
CAGCTGTTGGTGTCCAGGAGGTGATGGAGCCACTCCCACTGTT
810 820 830 840 850 X

15. US-09-030-606-174 (1-1459)
US-09-020-747-44 Sequence 44, Application US/09020747

Initial Score	=	69	Optimized Score	=	267	Significance	=	0.48
Residue Identity	=	34%	Matches	=	300	Mismatches	=	540

850 860 870 880 890 900 910
 ATAGCCTA-CTGTTGACGGGGAGCCTTACCAATAACATAAATAGTCGATTTATGCCATACGCTTTTATGCATTC
 450 460 470 480 490 500 510 520
 CTACAGTATCATTTTACAGTTTCCCAACACATTTGAAACAACAGTAGAAAATGATGAGTTGATTTTATTTATATGC
 920 930 940 950 960 970 980
 ATGATATACCTTTGTGGAAATTTTGTGATTTCTTAAGCTACACAGTTC--GTCTGTGAATTTTTTTTAAATTT
 530 540 550 560 570 580 590
 ATTACATCTCAAGAGTTTATACCAACCCCTCAGTTTATPAAAAATTTTCAAGTTATATTAGTCATATAAAGTT
 990 1000 1010 1020 1030 1040 1050
 GTTGCAACTCTCTAAATTTTCTGATGTGTTTATGAAAAATCCCAAGTATAGTGGAGCTGTGTCATTC
 600 610 620 630 640 650 660
 GGTGTGCTTATTTAAATTAGTCTGAATGGATTAGTGAAGACACAACATGTCCTCCCTTAATGTGATGATAT
 1060 1070 1080 1090 1100 1110 1120
 AACCAGGGTTGTTCAAGGGTCAACTGTGTACCCAGAGG----GAACAGTGACACAGATTCATAGAGGTGAA
 670 680 690 700 710 720 730
 TGGTCATTTTACCAGCTCTTAATCTTCACTTTTCAGGCTTTTGAAGTGAACATCTGNNATNACAGTGTTC
 1130 1140 1150 1160 1170 1180 1190
 ACACGAAGAGAAACAGGAAAAATCAAGACCTACAAAGAGGCTGGCAGGCTGGCTCATCGCTGTAATCCCA
 740 750 760 770 780 790 800
 NAGTTNCAACCTACTGGAACATTTACAGTGTGCTTGATTCAAAATGTTATTG--TTAAAAATTAATTTTA
 1200 1210 1220 1230 1240 1250 1260
 GCACTTTGGAGGCGAGCGGACGATCACTTGAGGTAAAGAGTTCAAGACCGCTGGCGCAAAATGGTGAA
 810 820 830 840 850 860 870
 ACCTGTGGGAAAAATTAATTTGAAATNA
 1270 1280 1290 1300 1310 1320 1330
 ATCTT
 1340 1350 1360 1370 1380 1390 1400
 AGTCGGGGGCTGACCCAGAGCTGCGTCCAGGAGAAATGCCTACCGTCTCGAGTGGCTGAAAGCTGTC
 410 420 430 440 450 460 470 480
 GGTGTGCTCANGAGGTCTGCANTAAAGCTCTATGACCCGCTCTACACCCCNACATGTTCTCGCGCGCGG
 1410 1420 1430 1440 1450 1460 1470 1480
 GATGAAATTTTAAAGCTTTTACATGTGATAGCACATAGTTTAAATTCGATCCCAAGTACTAACAAAACCT
 30 40 50 60 70 80 90
 1490 1500 1510 1520 1530 1540 1550
 AGGGCAAGACACAGAGGACTCCTGACCGTGAAGGGGGAAGGGGAGGCGGACATCGAGGGAAGGGT
 1560 1570 1580 1590 1600 1610 1620
 CTGAAATCAAGAATGGCAGCATGTTATTTATCAACATCAACACCTGTGGCTTTTAAAAATTTGGTTTTCAT
 100 110 120 130 140 150 160
 1630 1640 1650 1660 1670 1680 1690
 GAGAAGGGGGACAGACAGACACAGGCGCGCATGCGGAGATGCGAGATGGAGAGACACAGGAGGACAG
 170 171 172 173 174 175 176
 AAGATAATTTATACCTGAAGTAATCTAGCCATGCTTTTAAAAATGCTTTAG-GTCACCTCCAAGCTTGGCAG
 177 178 179 180 181 182 183
 184 185 186 187 188 189 190
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19. US-09-030-606-174 (1-1459)
US-09-020-747-17 Sequence 170, Application US/09020747

Initial Score = 61	Optimized Score = 90	Significance = 0.37
Residue Identity = 37%	Matches = 100	Mismatches = 166
Gaps = 3	Conservative Substitutions = 0	

GGTCAAGCCACACATGTTTCCAGAAAGTGAAGTGCAGAGCTCTCTACACATCGGGCTGGCCCTGCACAGTCTTGG
10 20 X 30 40 50 60 70
AGGCCACCAAGACCGGAGCGAGTGGTGGAGCCAGCTCTCCGTCAGCCACCCAGAGTACACAGAC
80 90 100 110 120 130 140
AGTGAGCTCAAGAGCTCTGCAGG--CATTTTGGCCAAACCTCTCCANAGCANAGGAGCAACCTCACTACTG

1270
ATCCT

1200
GCATTTGGAGCGGAGCGAGCGACATCTGAGGTAAAGGTTCAGACCGCTCGCCCAAAATGGTGGA
1210 1220 1230 1240 1250 1260
ACAGAGAGAACAGAGAAAATCAAGACTCTACAGAGCGCTGGCAGGCTGCTAGCTGCTAATCCCA
1130 1140 1150 1160 1170 1180 1190
NAGTTNCAACTACTGGAACATTCAGAGTGCCTGTCAAAATGTTATTGG--TAAAAAATTAATTTTA
740 750 760 770 780 790 800
TGTCATTTTACCAGCTCTAAATCTNAACTTCAGGCTTTTGAACTGGAAACATGATNANACAGTGTCCA
670 680 690 700 710 720 730
AACCAGGCTGTTCAAGGTCACCTGTACCCAGAG---GAAACAGTGACACAGATTCATAGAGGTGAA
1060 1070 1080 1090 1100 1110 1120
GTTGCACTCTCTAAATTTTCTGATGTTTATGAAAAATCCAAAGTATAGTGGAGCTGTGCATTCA
990 1000 1010 1020 1030 1040 1050
GTTGCTGCTATTTAAATAGTGTAAATGATTAAGTGAAGCAACAATGGTCCCTAAATGATGATAT
600 610 620 630 640 650 660
ATTACATCCTCAAGAGTTATCAACACCCCTCAGTTTAAAAATTTCAAGTTATATATTAGTCATATACCT
530 540 550 560 570 580 590
ATGATATACCTTTGTGGAAATTTTGTATTTCTAAGCTACACAGTTC--GTCTGTGAATTTTTTAAT
920 930 940 950 960 970 980
ATAGCCTA-CTGTGACGGGAGCCTTACCATAACATAATAGTCATGATTTATGCTATAGTTTATGATTC
850 860 870 880 890 900 910
CTATAGTATCATTTACAGTTTCCACACATTTGAAACAGTGAAGTCAAGTTTCAAAGTATAGGACAGAGTT
450 460 470 480 490 500 510 520
TCTATGCAAAATATGTCTAGCACTTTGATTCACCTCAGCCTGCACATTCAGTTTCAAAGTATAGGACAGAGTT
380 390 400 410 420 430 440
AATCATATACAGTATAAAGGAAAGGTGGTAGTGTGATGAAGAGT--TATTAGAATAGAATACTTGGCC
310 320 330 340 350 360 370
AAACGAAACAGACATGGGAGGAGGAGAAACACACATAGAAATGCAGTTGACCTTCCAAACAGCATGGGG
700 710 720 730 740 750 760
TTAACTTTGGCAFAACAATAATAAAACAATCACAAATTAATAAATAACAAATACAA--CATTTGTAGGCCAT
240 250 260 270 280 290 300

19. US-09-030-606-174 (1-1459)

Initial Score	=	61	Optimized Score	=	90	Significance	=	0.3
Residue Identity	=	37%	Matches	=	100	Mismatches	=	166
Gaps	=	3	Conservative Substitutions	=	0			

GGTCAGCGCACACTGTTCCAGAAAGTGAGTCAGAGGTCCTTACACATCGGGCTGGCGCTGCACAGTCTTG
 10 20 X 30 40 50 60
 AGGCGGACCAAGAGCCAGGAGCCGATGGTGCCAGCGCTCTCGTAGCGGACCCAGAGTACACAGAC
 80 90 100 110 120 130 140
 AGGTGGAGCTCAAGAGGCTCTGCAGG--CATTTGGCAANCCTCTCCANAGCAGGAGCAGCAACTACACTC
 X 10 20 30 40 50


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1150 1160 1170 1180 1190 1200
TCAAGACTCTACAAAGAGGTGGGAG-----GGTGGCTCATGCTGTATCCAGACACTTTGGAGGCG
1150 1160 1170 1180 1190 1200
GTCTTACGCCCCAGCTCTGGAAGCCACCCCTCTGCTGATCTGGTGGCCACACTCTCTTGAACACACATC
380 390 400 410 420 430 440

1210 1220 1230 1240 1250 1260 1270
AGGAGGAGATCACTTGGTTRAGGATTCAGACCCAGCTCGCCCAAAATG---GTGAAATCCTCTCTGTGA
1210 1220 1230 1240 1250 1260 1270
TCAAAATCCCACTCACCCCTCAAAACACCGCATGGGAGCCTTCTGACTTGGCTGATTTACTCCAGCATCTT
520 530 540 550 560 570 580

1280 1290 1300 1310 1320 1330 1340
CTAAATACAAAAGTTAGCTGGATATGTTGGCAGGCGCTGTAAATCCAGCTACTTTGGAGGCTGAGCAG
1280 1290 1300 1310 1320 1330 1340
GGAACAATCCCTGATCCCACTCTTAGAGGCAAGATAGGTTGTTAAGAGTAGGGCTGGACCACTTGGAG
590 600 610 620 630 640 650

1350 1360 1370 1380 1390 1400 1410
GAGAAATCTCTGAAT--ATGGGAGCAGAGTTGAAGTGAAGTGAATGATCAGACACACTATCTCCAGTGGG
1350 1360 1370 1380 1390 1400 1410
CCAGCTGCTGGCTTCAAAATTTGGCTCATTTACGAGCTATGGACCTTGGGCAAGTATCTTCACTTCTAT
660 670 680 690 700 710 720 730

1420 1430 1440 1450 X
CAACAGATTAAGACTCTGTCTCAAAAATAAAAAAAAAA
1420 1430 1440 1450 X
GGGCTCATTTTGTCTACCTGCAAAATGGGGGATAATAATAGT
740 750 760 770
```

22. US-09-030-606-174 (1-1459)
US-08-904-809-69 Sequence 69, Application US/08904809

Initial Score = 60 Optimized Score = 184 Significance = 0.36
Residue Identity = 38% Matches = 212 Mismatches = 324
Gaps = 18 Conservative Substitutions = 0

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10 20 30 40 50 60 70
GGTCAGCCGACACTGTTTCCAGAAGTAGTGAGCTCTTACACACTCGGGTGGGCTTGCACAGCTTGG
10 20 30 40 50 60 70
ACTAGTCCAGTGTGGGAATTCATTTGTTG
X 10 20 30

80 90 100 110 120 130 140
AGGCCGACCAAGAGCCAGGAGCCAGATGGTGGAGCCAGCTCTCCGTACGGCACCAGAGTACACAGAG
80 90 100 110 120 130 140
GGGCTCTCACCCCTCC-----TCTCTGAGCTCCAGCTTTTGTCTGTC-CTCTGAGGAGACCATGG
40 50 60 70 80 90

150 160 170 180 190 200 210
CCTTGTCTGCTAAGCACTCATGCTATCAAGTTGGACGAAATCCGTTCCGAGTCTGACACCATCCGGAGCA
150 160 170 180 190 200 210
CCAGCATCTGAGTACCCCTGCTCTCTGCTGGCCACCCTAGTGTGGCCCTGGGCTGGAGC--CCCAAGGA
100 110 120 130 140 150 160

220 230 240 250 260 270 280
TCAGATTGCTTCCAGTGTGCTGCGCTTCTCAAGGAGGTCTCTGCCCAGTCCGCGGCTGACCCAGAGCT
220 230 240 250 260 270 280
GGAGATAGGATAATCCCG--GGTGGCATCTATAACGAGCCACCAAGATGACTACTACAGACGTCCTGCGGTACTAAGAG
170 180 190 200 210 220 230

290 300 310 320 330 340 350 360
GTGAGCTCACGGGTGTGCTGCGCTTCTCAAGGAGGTCTCTGCCCAGTCCGCGGCTGACCCAGAGCT
290 300 310 320 330 340 350 360
ACTTCGCCATCAGCGAGTATACAGGCCACCAAGATGACTACTACAGACGTCCTGCGGTACTAAGAG
240 250 260 270 280 290 300 310
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CTGGTCCAGGAGATGCTACCGTGTGCTGAGTGGTGAACGCTGCTGGTGTCTCTGANGAGGTCTGCAN
110 120 130 140 150 160 170
CCAGGCAACAGACCG-----TTGGGGGGTGAATTTACTTCTTCGACGTAGAGTGGCGGCAACCATATGTAC
310 320 330 340 350 360 370

440 450 460 470 480 490 500
TAAGCTCTATGACCCGCTGACACCCCAACATGTTCTGCGCGCGGGAGGCAACACAGAGGACTCTCTG
440 450 460 470 480 490 500
CAAGTCCAGCCCACTTGGACACTGTGCTTCCATGAACAGCCAGAACTCGAGAGAAACAGTGTGCTC
380 390 400 410 420 430 440

510 520 530 540 550 560 570
CAAGCTGAGAGGGGAAAGGGGAGGAGCCGACTCAGGAAGGTGGAGAAAGGGGAGACAGACACAC
510 520 530 540 550 560 570
TTTCGAGATCTACGAAGTTCCTCGGGAGAACAGAAAGTCCCTGGGTGGAATCAGGTGTCAAGAAATCTTA
450 460 470 480 490 500 510

580 590 X 600 610 620 630 640
AGGGCCGATCGGAGATGAGAGATGGAGAGACACACAGGAGACAGTACACTAGAGAGAGAA
580 590 X 600 610 620 630 640
NGGATCTGTGTCAGGC
520 530 X
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23. US-09-030-606-174 (1-1459)
US-09-020-747-69 Sequence 69, Application US/09020747

Initial Score = 60 Optimized Score = 184 Significance = 0.36
Residue Identity = 38% Matches = 212 Mismatches = 324
Gaps = 18 Conservative Substitutions = 0

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10 20 30 40 50 60 70
GGTCAGCCGACACTGTTTCCAGAAGTAGTGAGCTCTTACACACTCGGGTGGGCTTGCACAGCTTGG
10 20 30 40 50 60 70
ACTAGTCCAGTGTGGGAATTCATTTGTTG
X 10 20 30

80 90 100 110 120 130 140
AGGCCGACCAAGAGCCAGGAGCCAGATGGTGGAGCCAGCTCTCCGTACGGCACCAGAGTACACAGAG
80 90 100 110 120 130 140
GGGCTCTCACCCCTCC-----TCTCTGAGCTCCAGCTTTTGTCTGTC-CTCTGAGGAGACCATGG
40 50 60 70 80 90

150 160 170 180 190 200 210
CCTTGTCTGCTAAGCACTCATGCTATCAAGTTGGACGAAATCCGTTCCGAGTCTGACACCATCCGGAGCA
150 160 170 180 190 200 210
CCAGCATCTGAGTACCCCTGCTCTCTGCTGGCCACCCTAGTGTGGCCCTGGGCTGGAGC--CCCAAGGA
100 110 120 130 140 150 160

220 230 240 250 260 270 280
TCAGATTGCTTCCAGTGTGCTGCGCTTCTCAAGGAGGTCTCTGCCCAGTCCGCGGCTGACCCAGAGCT
220 230 240 250 260 270 280
GGAGATAGGATAATCCCG--GGTGGCATCTATAACGAGCCACCAAGATGACTACTACAGACGTCCTGCGGTACTAAGAG
170 180 190 200 210 220 230

290 300 310 320 330 340 350 360
GTGAGCTCACGGGTGTGCTGCGCTTCTCAAGGAGGTCTCTGCCCAGTCCGCGGCTGACCCAGAGCT
290 300 310 320 330 340 350 360
ACTTCGCCATCAGCGAGTATACAGGCCACCAAGATGACTACTACAGACGTCCTGCGGTACTAAGAG
240 250 260 270 280 290 300 310
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CTGGTCCAGGAGATGCTACCGTGTGCTGAGTGGTGAACGCTGCTGGTGTCTCTGANGAGGTCTGCAN
310 320 330 340 350 360 370

440 450 460 470 480 490 500
TAAGCTCTATGACCCGCTGACACCCCAACATGTTCTGCGCGCGGGAGGCAACACAGAGGACTCTCTG
440 450 460 470 480 490 500
CAAGTCCAGCCCACTTGGACACTGTGCTTCCATGAACAGCCAGAACTCGAGAGAAACAGTGTGCTC
380 390 400 410 420 430 440

370 380 390 400 410 420 430
CTGGTCCAGGAGATGCTACCGTGTGCTGAGTGGTGAACGCTGCTGGTGTCTGANGAGGTCTGCAN
370 380 390 400 410 420 430
CCAGGCAACAGACCG-----TTGGGGGGTGAATTTACTTCTTCGACGTAGAGTGGGCGGCAACCATATGTAC
310 320 330 340 350 360 370
```


[illegible]

24. US-09-030-606-174 (1-1459)

US-09-020-747-10 Sequence 109, Application US/09020747

Initial Score	-	59	Optimized Score	-	478	Significance	-	0.34
Residue Identity	-	36%	Matches	-	546	Mismatches	-	891
Gaps	-	59	Conservative Substitutions	-	0		-	0

GGCACGAGGCTGGCCAGGGCCTTGACGGAGCGGGGGCAGCCTGCCACGGGGGGCCCCCGGGCCTGGCCAT
10 20 30 40 50 60 70
X GGTCAGCCGCACACTGTTTCCAG
20

30 40 50 60 70 80 90
 AAGTGAAGTCGAGAGCTCCCTACACCATCGGGCTGGGGCTGTGCAGTCTTTGAGGGCCGACACAGAGCCAGCGGAGGC
 80 90 100 110 120 130 140 150 160
 GCCTCACTGAGGCAGGCGCTTGGCCCTTACCTTCGCGCGACAGTGCGAACCACTGTGCAGCACTAGTGGCTCTCTACCC
 100 110 120 130 140 150 160
 CAGATGGTGGAGGCCAGCCTCTCCCTTACGGCACCCAGAGAGTCAACAGACCCCTTGTCTCGCTAACCAACCTCATG
 150 160 170 180 190 200 210
 TGTGTTCTCTGGCGCTGGGCTGCGCGGCTGACCCGGGTTTGTACCACTCTGGCGGCAGCTCTCTCTCTGCATC

CTCATCAAGTTGACGATCCCGTGTCCGAGTGACACCATCCGGAGCATTGACTTCGCAGTCGCCCT
|||||
GACTTCATGTTTTACGGTGGCGGTCTTACACTTTCACGGTCAACAACAGCTGGGGCCCCAAGATCGTTC

[illegible]

GCCTCTTCAAGAGGTCTCTGCCAGTCGCGGGGCTGACCCAGAGCTCTGGTCCACGGCAAGATGGCT
GTGGCCACGAGGGGCTCTGAGGCCACGGGACAGTGACTTCCCAAGTATCTCTGGGGGGCGCTCTTCTACCGT

[illegible][illegible]

AAAGGGGAGCGCAGGCAGTCTAGGGAAGGTGGAGAAGGGGAGACAGACAGACACACAGGGCCGATGCCGAG
AAGTCGCTGGTGCTGCTCTCCCTGCATCTTCCCTGCTG - GCCAACCTCGCTGGTCAACTTGCCTCAT

600 610 620 630 640 650 660
 ATCGAGAGTGGAGAGACACACGGGAGAGCATCACAACCTAGAGACAGAACTGAGCAAGAACACAGACAATAA
 650 660 670 680 690 700 710
 TGGCATGTTCACTTACACATTCGGCAAGTACAGGGACACGGCTCTCTACTTGAAGGCGCAGCGGTTACCG
 670 680 690 700 710 720 730
 ACACAGGAATAAAGAGAGAACAGGAGAGAGAGAAACAGAAACAGACATGGGAGGCGAGAAACACACACACACAT
 720 730 740 750 760 770 780
 CCTCATCCGGGAATTCACATCTCGGCCCGCGCTGGCCCCGCTTTATCGTCACTCTCCACCTTGGCGCTCCT
 740 750 760 770 780 790 800
 AGAAATGCGATTGACCTTCCCAACAGCATGGGGCTGAGGGCGGTGACCTCCACCCAATAGAAAAATCCTCTTA
 790 800 810 820 830 840 850
 GGTACGCAATTTGTCAGGCAC--CCGGAGGCCCCAGCGTCTCCCGGCCCTCGAGCATTTCCGGGTT
 810 820 830 840 850 860 870 880
 TAACATTTGATCCCAAAACCTGACTAGAAATAGCTACTTTGACGGGAGCGCTTACCAAATAACATAAA
 860 870 880 890 900 910
 TACCTTT-----CTAAGGAAGCCGAGCGGAAGTGCTACACTGGGAATCCGTGC-----ATAAGAG

890 900 910 920 930 940 950
TAGTCGATTTATGCATACGTTTTATGCAATTCATGATATACCTTTGTTCGAATTTTTTGATATTTCTAAGCTA
920 930 940 950 960 970 980
ACATTTCTGCTGGCAGCGCTTAGGGACAGGGGGAGCGACTCCAGGCGTGTGAAGCGCAGGTCCTCCAGAG

CACAGTTCGTGCGAAATTTTTTTTAAATCTTGCAACTCCATAAATTTTTCTCATGCTGTTATTGA AAA
GTAGTCTGTT
GTGGACTTGGCAGCTCAAAACAGCTGGGCACATCCGGAGTAGTACAACAGCCCTGGAAGTGTCTGGAGCGGGAG
990 980 970 960 950 940 930 920 910 900 890 880 870 860 850

[illegible][illegible]

1150 1160 1170 1180 1190 1200 1210
AAATCAAGACTCTACAAGAGCGCTGGCAGGGTGG--CTCATGCTGTATCCCGACACTTTGGGAGCGAG
CAGGGAGATTTTCTCCTTAGAGTAGTGAAGGCTCATCTGGCGCTCGGCCGCCGACCTGTGGCTGTGCTCTTGAGG
1210 1220 1230 1240 1250 1260 1270

GCAGGCAGATCACTCTGGAGGTAAAGAGGTTCAGACCGCTGGCCAAATCGTGTCTGTACTATAA
 TCGAGCCCCATGTCATCTGGGCCACTGTCTAGGACCACTTTGGGAGTGTCTATCCCTTACAAACCCAGACATGCG

AATACAAAGTTAGCTGATATGTTGGCAGCGCGCTTAATCCAGCTACTTGGAGGCTCAGGCAGGAGA-
 CGGGTCTCTCCAGAACAGTCCCGCTCGGAGGATCAAGGCTTGATCCGCGCGCTTATCATCTCGAGG-
 1290 1300 1310 1320 1330 1340 1350
 1360 1370 1380 1390 1400 1410

1360 1370 1380 1390 1400 1410 1420
ATTGCTTGAATATGGGAGGACAGGTTGAATCAGTTGAGATCACACCATTACTCCAGCTGGGGCAACAG
GCTGCAGGGTCCTTGGGTAAACGGGACACAGCCCTCACCACCTCACAGATTCTCCACATCGGGGAATATA

[illegible]

72	710
71	700
70	690
69	680
68	670
67	660
66	650

29. US-09-030-606-174 (1-1459)

29. US-09-030-606-174 (1-1459)

Initial Score	=	55	Optimized Score	=	201	Significance	=	0.29
Residue Identity	=	37%	Matches	=	227	Mismatches	=	361
Gaps	=		Conservative Substitutions	=			=	0

800 810 820 830 840 850 860
AAATCCTCTTATAACTTTTGACTCCCAAAACCTGACTAGAAATAGCCTACTGTTGACGGGGAGCCTTACC
|||||

870
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TGTGAT

AATAACATAAAATAGTCGATTATGATCATACGTTTATGCATTCAGAACCCCTCTGTTTT
TGGGTCTCGTGCTC-CACCAATGATAGAAAAACATGGTGTGTAAT-TTGATAGCAATATTTGGAGATTACAGAGT

[illegible]

TTTCTAAGCTACACAGTTCGCTGTGAATTTTAAATTTGTTGCAACTCTCCATAAATTTTTCGATG-1000

TTTAGTAATTACCAATTACACAGTTAAAAAGAGATAATATATTCGAAGCANATACAAAATATCTTAATGAA

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GTTTATTGAAAAATCCCAAGGATAAAGGGACCTGGCGAATCATTCCTC
GATCAAGGCAGGAAAATGANTATACTAATTGACAATCGGAAAATCAATTTTAATGTGAATTGCACATTATCCC

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TTTAAAAGCTTTCAAAANAANAATTATTCAGCTCTANTTAATTCAAACAGCTGTTAAAAATGGATATCAGGATATA
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Year	1990	1991	1992	1993	1994	1995	1996	1997	1998	1999	2000	2001	2002	2003	2004	2005	2006	2007	2008	2009	2010	2011	2012	2013	2014	2015	2016	2017	2018	2019	2020	2021	2022	2023	2024	2025	2026	2027	2028	2029	2030	2031	2032	2033	2034	2035	2036	2037	2038	2039	2040	2041	2042	2043	2044	2045	2046	2047	2048	2049	2050	2051	2052	2053	2054	2055	2056	2057	2058	2059	2060	2061	2062	2063	2064	2065	2066	2067	2068	2069	2070	2071	2072	2073	2074	2075	2076	2077	2078	2079	2080	2081	2082	2083	2084	2085	2086	2087	2088	2089	2090	2091	2092	2093	2094	2095	2096	2097	2098	2099	2100																																																																																																																																																																																															
1990	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300	3310	

GGTAAGGAGCTTCAAGACCGCCTGGCCAAATGGTGAAATCCTGTCTGTACFAAAAAATACAAAAGTTAGCC

ATGCANGGAAAGCAGTGGAGTAGGGAGTANTCAAGGTCTTCGGGCTCTAAATCGCCGCTT

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CATATGGTGGCAGGGCGGCTGTAAATCCAGCTACTGGGAGGTCAGGCAGGAGTAATGCTTGAATATGGGA

GGTGTG--GCCTTGATCCTCTGGAGACAGCTGCCAGGGCTCTGTATATCCACAATCCCAGCAAGAT

	450	460	470	480	490	500
1380	1390	1400	1410	1420	1430	1440

GCAGAGGTTGAAGTGGATTGAGATTCACACCACTATACTCCAGCTGGGGCAACAGAGTAAGAACTCTGTCTCTC

AAGGGATGAAAAAGGCACACATGCTTGCCTTCCTTTGAGGAGACATTCACTCCCGC

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30. US-09-030-606-174 (1-1459)
US-09-020-747-46 Sequence 46, Application US/09020747

Initial Score	=	55	Optimized Score	=	201	Significance	=	0.29
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38. US-09-030-606-174 (1-1459)
US-09-020-747-98 Sequence 98, Application US/09020747

Initial Score = 54 Optimized Score = 161 Significance = 0.27
Residue Identity = 38% Matches = 185 Mismatches = 276
Gaps = 19 Conservative Substitutions = 0

AGTGGTCAAGCTGCGTGGTGTCTGANGAGTCTGCANTAAGCTTATGACCCGCTGTACACCCCANCA 460
400 410 420 430 440 X 450
|||||
AGTGACTTGTCTCTCCAAACAAA 20
X

470 480 490 500 510 520 530
TGTTCTGGCGGGGAGGCAAGAGGAGTCTCTGCAACGTGAGAGAGGGGAAAGGGGAGGCGAGG 530
|||||
CCCTTGATCAAGTTTGGGCACTGCAATCAGACCTATGCTAGTTCCTGTCTATCTATTCGCTACTAAATGC 90
30 40 50 60 70 80

540 550 560 570 580 590 600
GACTCAGGGAAGGTTGGAGAAGGGGAGACAGACACAGGCGCCCATGGCGAGATGACAGATGGAGAG 600
|||||
-----AGACTGGAGGGGACCAAAAGGGGCATCAACTCCAGCTGGATTATTATTGGAGCCTGCAATCTAT 150
100 110 120 130 140 150

610 620 630 640 650 660 670 680
ACACACAGGAGACAGTACACACTAGAGAGAGAACTGAGAGAAACAGAGAAATAACACAGGAATTAAGAG 680
|||||
TCCTACTTGTACGGGACTTTGAAGTGATTTCAGTTTCCCTCTACGGA--TGAGAGACTGGCTCAAGAATATCCTC 220
160 170 180 190 200 210 220

690 700 710 720 730 740 750
AAGCAAGAGAGAGAGAAACAGACACATGGGGGAGAGAAACACACACATAGAAATCGATTGAC 750
|||||
ATGCACTTTTGAAGCCCACTCTGAACACGCTGTTATCTAGTAGAAGAGAGAAATAAGTCAGAAATTT 300
230 240 250 260 270 280 290 300

760 770 780 790 800 810 820
TTCCACACATGGGCGCTGAGGGCGGTGACCTCCACCCATAGAAATCTCTTATAACTTTTGACTCCCC 820
|||||
TACCTGGAGAAAGAGGCTTTGGCTGGGA---CCATCCCATGAACCTCTCTTAAGGACTTT-----A 360
310 320 330 340 350 360

830 840 850 860 870 880 890
AAAACTGACTAGAAATAGCTACTGTGAGGGGAGCCTTACCATAACATAAATAGTCGATTATGAT 890
|||||
AGAAACTACACATGTGTATCTCCGCGGCTTTATGAACTGACCCCTTTTGGATAATCTTG 430
370 380 390 400 410 420 430

900 910 920 X 930 940 950 960
ACGTTTATGATCATGATATACCTTTGTTGGAATTTTGTATATTTTCTAAGCTACACAGTTCGCTGTGA 960
|||||
ACGCTCTGAATGCTCTCTGCGA 460
440 450 460

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39. US-09-030-606-174 (1-1459)
US-09-020-747-94 Sequence 94, Application US/09020747

Initial Score = 54 Optimized Score = 162 Significance = 0.27
Residue Identity = 36% Matches = 180 Mismatches = 305
Gaps = 14 Conservative Substitutions = 0

10 20 30 40 X 50 60 70
GGTCAGCGGCACACTGTTTCCAGAGTGAAGTGCAGAGCTCTACACCTCGGCTGGGCTGACAGCTTG 70
|||||
CCCTTTGAGGGGTAGGGTCCAGTTCC 20
X

80 90 100 110 120 130
AGGCCGACCAAGACCGAGGAG-----CCAGATGGTGGAGCCAGCTCTCCCTACGCGCACCCAGAG 130
|||||
AGTGGAGAGAAACAGCGCCAGGAGAAATGCGTGGCGGAGCTGANGCAGATTTCACCAAGTGCACCCAGGCGCTG 170
170 180 190 200 210 220 230

30 40 50 60 70 80 90 100
140 150 160 170 180 190 200
TACACACACCTTGTCTGCTTAAGAGCTCATGCTCATAGTTGGAGCAATCGTCTCCGAGTCTCAGACCC 200
|||||
GGCTATAGTCTCTGACCCCTCCAAAGAAAGAACACCTTCTGGGGACATGGGCTGGAGGAGGACCTAGAGG 170
110 120 130 140 150 160 170

210 220 230 240 250 260 270
ATCCGAGCATCAGCATTCGCTTCCAGTGCCTACCGGGGGAACCTTTCGCTCTGCTTCTGCTGGGCTCTG 270
|||||
CACCAAGGAGAGGCC---CCATTCGGGGCTGTTCCTCCAGAGGAAGGGAAGGGCTCTGTGTGCCCCCA 240
180 190 200 210 220 230 240

280 290 300 310 320 330 340 350
CTGGGGAAGGCTGAGCTCACGGGTGTGTCTTCAAGGAGGTCTCTGCCAGTTCGCGGGGGCTG 350
|||||
CGAGGAANAGCCCTGANTCTG--GGATCANACACCCCTTCACGTGTATCCCAACAATGCAAGTCTACC 310
250 260 270 280 290 300 310

360 370 380 390 400 410 420
ACCCAGAGCTCTGCTTCCAGGAGAAATGCTTACCTGCTGCTGAGTGCCTGACGTTCGGTGGTGTCTGANG 420
|||||
AAGTCCCTCTCAGTCTTCCCTTACACCTTGAACGNCACCTGGCCCCACACCCACCCAGANCAACCCCG 380
320 330 340 350 360 370 380

430 440 450 460 470 480 490
AGGTCTGCANTAAAGCTCTATGACCCGCTGTACCCCCANCATGTTCTGCGCGCGGAGGCGAAGACCAGA 490
|||||
CCATGGGGAATGCTCTAGGAATGCGGCGGCACTGCTCTGCTCCNNAAGGGGCAAGATCTCCAAT 450
390 400 410 420 430 440 450

500 510 520 530 X 540 550 560
AGACTCTCTGCACTGAGAGAGGAGGGAAGGGGAGGCGGCTCAGGGAAGGCTGAGGAAGGGGAGAG 560
|||||
AGANGGANNAGACCCCTTGTCTNANAAAAAANAANAANA 490 X
460 470 480 490

570 580
AGAGACACACAGGCGCG

40. US-09-030-606-174 (1-1459)
US-09-020-747-14 Sequence 145, Application US/09020747

Initial Score = 52 Optimized Score = 104 Significance = 0.25
Residue Identity = 40% Matches = 125 Mismatches = 176
Gaps = 10 Conservative Substitutions = 0

900 910 920 930 940 X 950 960
TGCATACGTTTATGCAATTCATGATATACCTTTGTTGGAATTTTGTATATTTCTAAGCTACACAGTTCGTC 960
|||||
ACGTAGACCATCCAATTTGTA 20
X

970 980 990 1000 1010 1020 1030
TGGAATTTTTTAAAT--TGTTGCAACTCTCTAAATTTTCTGATGTTTATGAAAATCCAGTA 1030
|||||
TTTCTAATGCAAACTCCAGNAGCAATCTTAAACAACTGGAGGCTATTTATACCCCAATTTATCCCATCA 90
30 40 50 60 70 80 90

1040 1050 1060 1070 1080 1090 1100
TAAGTGCACTGTGCAATTCAAACAGGCTTGTTCAGGGTCAACTGTGTACCCAGAGGGAACAGTACACA 1100
|||||
TTAATATGCTCTCTCTCAGGTATGAGG---ACAGCTATCATTAAGTGGCCGAGGATCCAGATATAC 160
100 110 120 130 140 150 160

1110 1120 1130 1140 1150 1160 1170
GATTCTAGAGGTGAACACAGAGAGAAACAGGAATACTCAAGACTCTACAAAGGCTGGCGAGGTGGCT 1170
|||||
CATTTGTATAAATCTTCAAGTGGGAGTCCATCCCAAGTACAGGTCTAATCAAA---GGAGGAATGGACAT 170
170 180 190 200 210 220 230

80 90 100 110 120 130 140 150

CTTTGAAGAAGGGATGGCTC
X 10 20

15. US-09-030-606-174 (1-1459)
US-08-904-809-3 Sequence 3, Application US/08904809

45. US-09-030-606-174 (1-1459)
US-08-904-809-3 Sequence 3, Application US/08904809

Initial Score	=	48	Optimized Score	=	250	S
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720	730	740	750	760	770	X
880	890	900	910			
TAACATAAATAGTCGATTATGATACAGTTTTATGCAATTC						

46. US-09-030-606-174 (1-1459)
US-09-020-747-3 Sequence 3, Application US/09020747

Initial Score	=	48	Optimized Score	=	250	Significance	=	0.19
Residue Identity	=	35%	Matches	=	282	Mismatches	=	491
Gaps	=		Conservative Substitutions	=			=	0

10	20	30	40	50	60	70
CGCACACTGTTTCCAGAAGTGAGTGCAGAGCTCCTACACCATCGGCTGGCGCTGCACAGTCTTTGAGGCGCGA						
CTTTTGAAGAAGGATGGCTG						
X						
80	90	100	110	120	130	140
CCAAGAGCCAGGGAGCCAGATGGTGGAGGCGAGCCTCTCCGTACGGCAGCCAGAGTACAAACAGACCCCTGTCT						
150	160	170	180	190	200	210
GGGTGTTTAAACAGACAGAGGTGCAGGGCGGGGCTCAGCTCTCTCTCACTGGTGATAAACAGAGCCCGCTT						
220	230	240	250	260	270	280
CGCTAAACGAGCTCATGCTCATCAAGTTGGAGCAATCCGTCTCCGAGTCTGACACCACTCCGGAGCATCAGCAT						
290	300	310	320	330	340	350
CCTGTGTTGATCATGATGATACACACTCTCTCAAAAGTACAGACCGGAGTACACAGAGCATCTGTGCCGCTCA						
360	370	380	390	400	410	420
TGCTTTCAGTGCCTACCGGGGAACTCTTGCTCTGCTTCTGGCTGGGTCTGCTGGGCAACGGTGAGCT						
430	440	450	460	470	480	490
AGATTCACACCACTCTGCCTTCGTCTCTTTCGAATATCATCTGCAAACTCTCTTCTCATTTCTTGCCCAAT						
500	510	520	530	540	550	560
CACGGGTGTGTCTGCTGCCCTTCTCAAGGAGTCTCTGCCAGTGCGGGGGCTGACCCAGAGAGTCTGCGCTC						
570	580	590	600	610	620	630
CA-----TCCATGCTCATCTGATTGGGAAGTTCATCAGACTTTAGTCCANNCTCTTCTGATCAGCAGC						
640	650	660	670	680	690	700
CCAGGCAGATGCTTACCGTGTGACGTGCGTGAACGTGTCGGTGGTGTCTGANGAGGTCTGCANTAAAGTCT						
710	720	730	740	750	760	770
TCGTAGA-----ACTGGGGTCTATTGCTCCACAGCCATGAATTCCTCCCTCTGCTGCTGTGAAGTCT						
780	790	800	810	820	830	840
440 450 460 470 480 490 500 510						
TATGACCGCTGTACCAACCCANCATGCTTGGCGCGGAGGAGGCAAGACCAAGAGGACTCTCTGCAACGTG						
850	860	870	880	890	900	910
TATAGAAGGTGCTCCACCATCCAAACATGTTCTGCTCCTCAGGGGGCGCGGTACCCAATTTCGCCCTATAT						
920	930	940	950	960	970	980
AGAGAGGGGAAAGGGAGGCGAGCGAGTCTGAGGAAGGGTGGAGAGGGGAGACAGACAGACACAGCGGGCG						
990	1000	1010	1020	1030	1040	1050
TGAGTCGTATTACGCGGCTCACTGGCC-----GTGCTTTTACAACGTCGTGACTGGGAAACCCCTGGCG-						
1060	1070	1080	1090	1100	1110	1120
CATGGCAGATGCAGAGATGGAGAGACACACAGGAGACAGTGCACAATAGAGAGAAACTGTAGAGAAACA						
1130	1140	1150	1160	1170	1180	1190
-----GTTTACCAACTTAATCGCTTGCAGACATCCCTTCGCCAGCTGGCGGTATATACGAAAGGCCCGC						
1200	1210	1220	1230	1240	1250	1260
GAGAAATAAACACAGGAATAAGAGAGCAAGAGAGAGAGAAACAGAAACAGACA"GGGGAGCGCAAGAAACA						
1270	1280	1290	1300	1310	1320	1330
CACGATTCGCGCCCTTCCA--ACAGTTGCGCACCTGAATGGGNAATGGGACCCCTCTTTACCGCGCATTTNAA						

710
CATGGGAGGCAGAAACACACACATAGAAAATGCAGTTGACCTCCACACCATTGGGGCCTGAGGGCGGTG

CCCCCTAATCCAGCTACTTGGGAGGCTGAGCGAGGAGA
1320 1330 1340 1350

920 930 940 950 960 970 980 990
ACCTTTGTGGAAATTTTGTATATTTCTAAGCTACACAGTTCGTCGTGAATTTTTTAAATTTGTGCAACT


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1000 1010 1020 1030 1040 1050 1060
CTCCATAAATTTTCTGATGTTTATTGAAATAATCAAGTATTAAGTGACCTTGTGATTCAACACGAGGT
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TGGTTTGCTATAGCCGAGGACCTTTGACAGAACAAAGAGGACTTCGAGTAAGAAGGTGATTTACAGC
1200 1210 1220 1230 1240 1250 1260
TGTTCAGGGTCAACTGTGTACCCAGAGGAACAGTGACACAGATCATAGAGGTGAACACGAGAGAAA
1300 1310 1320 1330 1340 1350
CAGCCTAGTGCAGGAGGAGGAATTCACACAGAGCTCGTCAATCT-GGTGTGAGCCTGTGTGAGTT-
1400 1410 1420 1430 1440 1450 1460
1140 1150 1160 1170 1180 1190 1200
CAGGAAATCAAGACTCTACAAAGAGGCTGGCAGGTGCTCAAGTGTAAATCCAGCACTTTGGGAGG
1210 1220 1230 1240 1250 1260 1270
CGGCTATCATCTGATTTGCTTACTAGGTGCTACGGGACTCTGCGCCCTGATGTCTGTGTTT-----
1280 1290 1300 1310 1320 1330 1340 1350
TAAATAACAAAGTTAGTATGTTGGCAGGCGCTGTAAATCCAGCTACTTGGGAGGCTGAGGAGG
1360 1370 1380 1390 1400 1410
AATAATGTCAGTATGTGCCCATCTCTTCATGCTCCCTCCCTTCTTCCAGCACTGCTGAGTGGGCTGG
1420 1430 1440 1450 1460 1470
300 310 320 330 340 350 360
-----CACAGATGCTTATTGTCTTCTACACCCACAGGCGCCCTTCTTCCGATGTGTTTT
1480 1490 1500 1510 1520 1530 1540
1210 1220 1230 1240 1250 1260 1270
CGAGCAGGAGATCCTAGGTAGGTAAGGATTCACAGACAGCTCGCCAAATGGTGAATCCTCTGTGATC
1550 1560 1570 1580 1590 1600 1610
-----CACAGATGCTTATTGTCTTCTACACCCACAGGCGCCCTTCTTCCGATGTGTTTT
1620 1630 1640 1650 1660 1670 1680
1280 1290 1300 1310 1320 1330 1340 1350
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1690 1700 1710 1720 1730 1740 1750
AATAATGTCAGTATGTGCCCATCTCTTCATGCTCCCTCCCTTCTTCCAGCACTGCTGAGTGGGCTGG
1760 1770 1780 1790 1800 1810 1820
300 310 320 330 340 350 360
-----CACAGATGCTTATTGTCTTCTACACCCACAGGCGCCCTTCTTCCGATGTGTTTT
1830 1840 1850 1860 1870 1880 1890
1360 1370 1380 1390 1400 1410
AGAANTGCTGAATATGGAGGACAGAGTTGAAGTGAAGTGAATGATACACCACTATACTCCAGTGG
1900 1910 1920 1930 1940 1950 1960
AACTTGTAAAGTGT
370 380 X
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51. US-09-030-606-174 (1-1459)

US-08-904-809-72 Sequence 72, Application US/08904809

```
Initial Score = 47 Optimized Score = 170 Significance = 0.18
Residue Identity = 37% Matches = 191 Mismatches = 310
Gaps = 10 Conservative Substitutions = 0

320 330 340 350 360 370 380
TCAAGGAGTCTCTGCTCCAGTGCAGGCGGTGACCCAGAGCTCTGCTCCAGGCAAGTCCCTACCGTGC
390 400 410 420 430 440 450 460
TGCAGTGGCTGAACGTGCGGTGCTGTGANGAGGTCTGCANTAAGCTTATGACCGCTGTACACCCCA
470 480 490 500 510 520 530
NCATGTTCTGCGCGGAGGAGGCAAGGAGTCTCTGCAACGTGAGAGGAGGAGGAGGAGGCA
540 550 560 570 580 590 600
GGCG--ACTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
610 620 630 640 650 660 670
GAGAGAGTGTGGAACATGAGAGATGTTGCTGGANATCGCGGTGCTTCTTCTTCTTCTTCTTCTTCTT
680 690 700 710 720 730 740
170 180 190 200 210 220 230
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750 760 770 780 790 800 810
610 620 630 640 650 660 670
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780 790 800 810 820 830 840
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850 860 870 880 890 900 910
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920 930 940 950 960 970 980
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990 1000 1010 1020 1030 1040 1050
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1060 1070 1080 1090 1100 1110 1120
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1130 1140 1150 1160 1170 1180 1190
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1200 1210 1220 1230 1240 1250 1260
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9460 9470 9480 9490 9500 9510 9520
GAGAGAGTGTGGAACATGAGAGATGTTGCTGGANATCGCGGTGCTTCTTCTTCTTCTTCTTCTTCTT
9530 9540 9550 9560 9570 9580 9590
GAGAGAGTGTGGAACATGAGAGATGTTGCTGGANATCGCGGTGCTTCTTCTTCTTCTTCTTCTTCTT
9600 9610 9620 9630 9640 9650 9660
GAGAGAGTGTGGAACATGAGAGATGTTGCTGGANATCGCGGTGCTTCTTCTTCTTCTTCTTCTTCTT
9670 9680 9690 9700 9710 9720 9730
GAGAGAGTGTGGAACATGAGAGATGTTGCTGGANATCGCGGTGCTTCTTCTTCTTCTTCTTCTTCTT
9740 9750 9760 9770 9780 9790 9800
GAGAGAGTGTGGAACATGAGAGATGTTGCTGGANATCGCGGTGCTTCTTCTTCTTCTTCTTCTTCTT
9810 9820 9830 9840 9850 9860 9870
GAGAGAGTGTGGAACATGAGAGATGTTGCTGGANATCGCGGTGCTTCTTCTTCTTCTTCTTCTTCTT
9880 9890 9900 9910 9920 9930 9940
GAGAGAGTGTGGAACATGAGAGATGTTGCTGGANATCGCGGTGCTTCTTCTTCTTCTTCTTCTTCTT
9950 9960 9970 9980 9990 10000
GAGAGAGTGTGGAACATGAGAGATGTTGCTGGANATCGCGGTGCTTCTTCTTCTTCTTCTTCTTCTT
10010 10020 10030 10040 10050 10060 10070
GAGAG
```



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53. US-09-030-606-174 (1-1459)
US-08-904-809-4 Sequence 4, Application US/08904809

Initial Score = 47 Optimized Score = 264 Significance = 0.18
Residue Identity = 34% Matches = 292 Mismatches = 533
Gaps = 19 Conservative Substitutions = 0

      250      260      270      280      290      X      300      310
GGGGAACCTTTGCCCTCGTTTCTGGCTGGGCTGTCTGGGCAACGTGAGCTCACGGGTGTGTCTCTGCCTC
      |||      |||      |||      |||      |||      |||      |||
      CCTCTGAGTCCTACTGACCTG      X      10      20

      320      330      340      350      360      370      380
TTTCAAGGAGGTCCTCTGCCACTCGCGGGGCTGACCCAGAGCTCTGGTCTCCAGGCAGAAATGCTTACCGTG
      |||      |||      |||      |||      |||      |||      |||
      TGCCTTTCGGTGTGGAGTCCA---GGGCTCTCTAGGAAAAGGAATGGGCAGACACAGGTGTATGCTCAATGTTT
      30      40      50      60      70      80

      390      400      410      420      430      440      450      460
CTGCAGTCGGTGAACGTCTCGGTGGTCTCTGANGAGGTCTGCANTAAGCTCTATGACCCGCTGTACCAACCCC
      |||      |||      |||      |||      |||      |||      |||
      CTGAATGGGTATA-----ATTTCGCTCTCTCCTCGGAACTAGCTGTCTCTCTCAAGACATTCTCG
      100      110      120      130      140      150

      470      480      490      500      510      520      530
ANCATGTTCTCGCGCGGAGGCGACACAGGAGAC--TCCTTCAACGTTGAGAGAGGAAAGGAGGAGG
      |||      |||      |||      |||      |||      |||      |||
      CTGAGTTCAGTGAAGACACACAAAGACGTGGGTGACCATGTTGCTTTGTGGGTGCAGAGATGGGAGGG
      160      170      180      190      200      210      220

      540      550      560      570      580      590      600
GCAGGCGCACTCAGGGAAGGTTGAGAAGGGGGAGACAGACACACAGGCGCCGATGGCGAGATGCAGAGAT
      |||      |||      |||      |||      |||      |||      |||

```

54. US-09-030-606-174 (1-1459)
US-09-030-747-4 Sequence 4. Application US/09020747

Initial Score	=	47	Optimized Score	=	220	significance	=	0.18
Residue Identity	=	34%	Matches	=	264	Mismatches	=	466
Gaps	=		Conservative Substitutions	=	25		=	0

[illegible]

TCATTATAACATTTTGGCTCCCAAAACCTGACTAGAAATAGCCTACTGTTGACGGGAGCGCTTACCAATAAAC
CTGAATGGGTATAATTTGGTCTCTCTCTCGCTTCGGAACACTGGCTGTCTCT-----GAAGACTTCTTCGCTCAG
100 110 120 130 140 150

880 890 900 910 920 930 940
ATAAATAGTCGATTTATGCAATACGTTTTATGCAATTCATGATATACCTTTGTGGAATTTTTTGATATTTCTTA
TTTCAGTGGAGCACACACACA -AAGACCTGGGTGACCATGTTGTTTGGGTGCAGAGATGGGAGGGGTGGG
160 170 180 190 200 210 220

950 960 970 980 990 1000 1010
AGCTACACAGTTTCGCTGTGGAATTTTTTAAATTTGTCCAATCTCCCTAAAAATTTTTTCTGATGTTTATTATGG
GCCACCTCTGGAAG--AGTGGACAGTGACACAAGGTGGACACTCTCTACAGATCACTGAGGATAAAGCTGGAG
230 240 250 260 270 280 290

1020 1030 1040 1050 1060 1070 1080 1090
AAAAATCCAAAGTATAGTGGACCTGTGCAATTCAAACCAAGGCTGTTCAAGGGTCAACTGTGTACCCAGAGG
CCAAATGCATG-----AGGCACACACACGAAGGATGACNCTGTGTAACATAGCCACGCTGTCTCTGNG
300 310 320 330 340 350 360

1100 1110 1120 1130 1140 1150 1160
GAAACAGTGACAGACATTCATAGAGTGGAAACCGAAGAGAAACAGGAAAAATCAAGACTCTACAAAGAGGC
GGCACTGGGAAGCTTANATNAGSCCTG-AGCANAAAGAAAGGGAGGATCCACTAGTTCTANAGCGCGCCGC
370 380 390 400 410 420 430

1170 1180 1190 1200 1210 1220 1230
TGGCGAGGTTGGCTCATGCTGTAATCCCAAGCACTTTGG-----AGGCGAGCGAGGAGCATCACTTGGAGTA
ACCAGCTGGCACTCCANCTTTTGTTCCTTTAGTGAGGGTTAATTGCGCGTGGCCTATCATGTCATCA
440 450 460 470 480 490 500

1240 1250 1260 1270 1280 1290 1300
AGGAGTTTCAAG-ACCAGCCTGGCCAAATGGTGAATCCTGCTGTACTAAAAATACAAAAGTTAGCTGGAT
NCTNTTCTGTGTGGAATTTGTTATCCGCTCACAATTCACACAACATACGACCGGAAACATAAANTGTAA
510 520 530 540 550 560 570

1310 1320 1330 1340 1350 1360 1370
ATGTTGAGCGAGCGCCTGTATATCCAGCTACTTGGAGGCTGAGGCAGAGAAATTCCTGTAATATGGGAGGCA
ACCTGGGGTCCCTTAATGANTGACTTAACATCAATTAATTCGCTTGGCCTCACTGCCCGCTTTTCCAATCNGAA
580 590 600 610 620 630 640 650

1380 1390 1400 1410 1420 1430 1440
GAGTTGGAAGTGAGTTGAGATCACACCATATCTACAGCTGGGGCAACAGAGTAAGACTCTGTCTCAAAA
ACCTGTCTGCCNCTTGCAATTNATGATCNGCCAAACCCCGGGGAAAAAGCGTTTGCCTTTTGGCGCTCTTC
660 670 680 690 700 710 720

1450 x
AAAAAAAAAAAA
CGCTTCTCCTCANTANTTCCCTNCNCTCGGTCTATTCGGGCTGCGCAAAACCGGTTTCAACGNC

55. US-09-030-606-174 (1-1459)

US-09-030-008-174 (1-1439)
US-09-020-747-19 Sequence 19, Application US/09020747

Initial Score	=	46	Optimized Score	=	216	Significance	=	0.16
Residue Identity	=	32%	Matches	=	238	Mismatches	=	486
Gaps	=	11	Conservative Substitutions	=	0			

150 160 170 180 190 x 200 210
CCCTTGCTGCTAACGACCTCATGCTCATCAAGTTGGAGCAATCGTCTCGAGTCTGCACACCATCGGAGC
CNAAGCTTCCAGGTTNACGGGCC

[illegible]

56. US-09-030-606-174 (1-1459)

36. US-09-030-606-1/4 (I-1459)
US-08-904-809-59 Sequence 59, Application US/08904809

Initial Score	=	45	Optimized Score	=	118	Significance	=	0.15
Residue Identity	=	38%	Matches	=	129	Mismatches	=	201
Gaps	=	8	Conservative Substitutions	=			=	0


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57. US-09-030-606-174 (1-1459)
US-09-020-747-59 Sequence 59, Application US/09020747

Initial Score = 45 Optimized Score = 118. Significance = 0.15
Residue Identity = 38% Matches = 129 Mismatches = 201
Gaps = 8 Conservative Substitutions = 0

          900   910   920   930   940   950   960   970   980   990
GTTTTATGCATTCAATGATATACCTTTGTTGGAAATTTTGTATATTTCTTAAGCTACACAGTTCGTCGTGGAAT
TTTAAAAATTTGTTGCAACTCTCCTAAATTTTCTCGATGCTTTATTGAAAAAATCCAAAGTATAAGTGTGCAC
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
GTCATTATCA-----GCAAAACTGGTGATGCTACTGAAAGAATCCATTGAAATTCATTAATGATTTTAA
30      40      50      60      70      80
1050   1060   1070   1080   1090   1100   1110
TTGTGCATCAAAACCGGGTTGTTCAAGGGTCAACTGCTGCCACGAGGAGAAACAGTGCACACAGATCATAG
|||||  |||||  |||||  |||||  |||||  |||||  |||||
ATGCAAGGTATATCAAAAACTCACTCAATTTTTCACCTGTG---CTAGCTTGCTAAATGGGAGTTTAACCTTAG
90      100     110     120     130     140     150

1120   1130   1140   1150   1160   1170   1180
AGGTGAACACAGAGAAACAGCAAAAATCAAGACTCTACAAAGAGCGGTGGCGAGGTTGGCTCATCGCGTGT
|||||  |||||  |||||  |||||  |||||  |||||  |||||
AGCAAAATATAGTATCTTCTGAAATACAGTCAATTAATGACAAAGCCAGGCGCTPACAGGTGGTTTCCAGACTTT
160     170     180     190     200     210     220     230

1190   1200     1210   1220   1230   1240   1250
AATCCACGACTTTTGGGAGGCGAGCGAGGAGATCACTTGAGGTAAGAGAGTTCAAGACACCGCTGGCGCAAA
|||||  |||||  |||||  |||||  |||||  |||||  |||||

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US-09-030-606-174 (1-1459)
US-08-904-809-19 Sequence 19, Application US/08904809

Total Score	=	45	Optimized Score	=	216	Significance	=	0.15
Residue Identity	=	32%	Matches	=	238	Mismatches	=	486
Gaps	=		Conservative Substitutions	=			=	0

59. US-09-030-606-174 (1-1459)
US-09-004-809-19 sequence 19. Application US/08904809

[illegible]

67. US-09-030-606-174 (1-1459)
US-09-030-747-15 Sequence 159. Application US/09020747

Initial Score	=	43	Optimized Score	=	162	Significance	=	0.12
Residue Identity	=	3%	Matches	=	180	Mismatches	=	314
Gaps	=		Conservative Substitutions	=	14		=	0

800 810 820 830 840 X 850 860
TAGAATACTCTATACCTTTGACTCCCAAAAGCTAGTAAATAGCTACTGTGTGACGGGAGCCT
ACTTCCAGGTAACTGTGTGT
X 10 20

TACCAATAACAATAAATAGTCGATTATGATCATCGTTTTTGCATATACCTTTGTGGAAATTTTT
870 880 890 900 910 920 930

[illegible]

1090 1100 1110 1120 1130 1140 1150
TATCCAGAGGAAACAGTGCACAGATTACAGGTGAACACAGAGAAACAGGAAAAATCAAGACTCT
1160 1170 1180 1190 1200
TTCAACAGGGGCGTGTGGTGGCCGGGAGCTGAAGCTTGTGTCACITTGAGCTTGGCCGACTTGTGAAGT

1160 1170 1180 1190 1200 1210 1220
ACAAAGAGCGTGGGAGGGTGGCTGCTGTAATCCAGCACATTGGGAGGCGAGCGAGATCACTT
ANTANATTCTTCTGAAGGCGAGCGCTTTGGAGCTGGCAGGGGTCANTTTGTGTGTAAACGACCACTGCT

1230 1240 1250 1260 1270 1280 1290
GAGTAAAGAGTTCAGA- ---CCAGCCTGCCCAATGTTGAATCTGCTGCTGTAATAAATAACAAAGT
GCTGTGGGTGGGTGTANATCTCCACAAAGCCTCAAGTTATGGTGTGTCNTCAGGTAAANAATGGTGTTCAGTG

	1300	1310	1320	1330	1340	1350	1360
TAGCTGATATGGTGGCAGCGCCGTGTAATCCACAGCTACTTTGGAGGCTTGACGAGGAATTGCTTGAATA							
TCCTGGCGNGCTGTGAAGAGTGTANATTGTCACCAGGGAATAAGCTGTGTG							X
+40	+50	+60	+70	+80	+90		

1370 1380 1390
TGGAGGCAGAGGTTGAAGTGAGTTGAGATCA

68. US-09-030-606-174 (1-1459)

US-08-904-809-74 Sequence 74, Application US/08904809

Initial Score	=	43	Optimized Score	=	190	Significance	=	0.12
Residue Identity	=	37%	Matches	=	211	Mismatches	=	326
Gaps	=		Conservative Substitutions	=	25		=	0

90 500 510 520 530 540 550 560
CCAGAGGACCTCCTCTGCACGTGACAGAGGGGAAAGGGGAGCGACTCAGGCAGAGGCTGAGAGGGG
TTTCATAGGAGGAAACACACTGA
x 20

[illegible]

GAGAGAGAACTGAGAGAACAGAGAAATAACACAGGTAATTAAGACAGAGCAAGGAGAGAGAAACAGAAA
- - - - -
AATAAGCTAAAGACTAGTCTCTAACTTCGAGGCCCGCTCAAGTGGAATTGGAATACTGCATTTTACAG----

710 720 730 740 750 760 770
CAGACATGGGGAGCAGAAACACACACATAGAAATGGAGTGTGACCTTCACAGCATGGGGCTGAGGGC
-----TGTACAGTAAACACATAACATTTGATGGATGGAACACATGGAGGACAGTATTACAGTGTCCC

[illegible]

850 860 870 880 890 900 910 920
TGTTCAGGGAGCCCTACCAATAACATAAATAGTCGATTTATGCATCATCTTTTATGCATTCATCATGATATACC
ATT----AGGCGCTTTGATTTATNACACTTTGGTGACTTATCAATAATTTGTTAGTTATCTAGCTGCTTCACAG
300 310 320 330 340 350 360

TTTGGTGGAAATTTTGGATATTTCTAAGCTACAGATTCGTCGTGAATTTTTTTAAATTTGTTGCAACTCTCT
TTTTTTT
TTTGGCTGATATATTTGTTGATATTTAAGATTCCTGACTATATTTTGAATGGTCTTACTGAAAANGAAT
TTTTTTT

CTAAAATTTTCTGATGGTTTATTGAAAAATCCAAAGTAACTGACCTTGTCATTCAAACGACGGTTG
ATATATCTTTGAAGACATCGATATACATTTATTACACTCTTGATTTTCACATGTAGAAAATCAAGS
500

440 430 420 410 400 390 380 370 360 350 340 330 320 310 300 290 280 270 260 250 240 230 220 210 200 190 180 170 160 150 140 130 120 110 100 90 80 70 60 50 40 30 20 10

TCAAGGTCACACTGTGTACCCAGAGGAAACAGTCACACGATTCTATAGAGGTGAACACACGAGAGAAACAC

-AAATGCCCCCAATTCGTATGGTGATAAAGATCCCGT

510 520 530 A

1140 1150
GAAATCAGACT

69. US-09-030-606-174 (1-1459)
US-09-020-747-74 Sequence 74, Application US/09020747

Initial Score	=	43	Optimized Score	=	190	Significance	=	0.12
Residue Identity	=	37%	Matches	=	211	Mismatches	=	326
Gaps	=		Conservative Substitutions	=	25		=	0

490 500 510 520 530 540 550 560


```

      570 580 590 600 610 620 630
GAGACAGACACACAGCGCGCATGGCGAGATGAGAGACACACAGGGAGACAGTCAACACTA
|||||
GAGATCTTGAAGAAATTTGGATTTCAGCGCGCGAAGAGATTTATCAGTTCACTCAGATAAAATCATTTGAAAGT
30 40 50 60 70 80 90
      640 650 660 670 680 690 700
GAGAGAGAACTGAGAGAAACAGAGAAATTAACACAGCAAGTAAGAGAGCAAGGAGAGAGAGAGAGAA
|||||
AATAGGTAAAGCTAGTCTCTAATCCAGCGCCACGGCTCAAGTGAATTTGAATCTGCATTTACAG---
100 110 120 130 140 150 160
      710 720 730 740 750 760 770
CAGACATGGGAGGAGAGAAACACACACATAGAAATGCAATGACCTTCCAAACAGCATGGGCTGAGGCG
|||||
-----TGTAGAGTACACATTAACATTTGATGCAATGGAAACATGGAGGACAGTATTACAGTCTCC
170 180 190 200 210 220
      780 790 800 810 820 830 840
GGTGACCTCCACCCCAATAGAAAATCTCTTATACTTTTGACTCCCCAAACCTGACTAGAAATAGCCTAC
|||||
TACCACTCTATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGTGATGATTAATCTTAAATATGGTAATC
230 240 250 260 270 280 290
      850 860 870 880 890 900 910 920
TGTTGACGGGAGCCTTACCATAACATAAATAGTCGATTTATGCTATCGTTTATGCTATCATGATATACC
|||||
ATT----AGGCGTTTGTATATAAATCTTTGGGTACTTATATCAATTAATTTAGTTTACTGCCTTCCAG
300 310 320 330 340 350 360
      930 940 950 960 970 980 990
TTTGTGGAATTTTGTATATTTCTAAGCTACACAGTTCGCTGTGAATTTTAAATTTGTGCAACTCTC
|||||
TTTGTGATATATTTGTGATATTAAGATTTCTGACTTATATTTTGAATGGTCTACTGAAANAANGATG
370 380 390 400 410 420 430
      1000 1010 1020 1030 1040 1050 1060
CTAAATTTTCTGATGTGTTTATTGAAATAATCAAGTATAAGTGGACTTGTGCTTCAACACAGGTTGT
|||||
ATATATTTTGAAGACATCGATATACATTTATTTACACTCTTGATCTTCAATGTAGAAATGAAG-----
440 450 460 470 480 490 500
      1070 1080 1090 1100 1110 1120 1130
TCAAGGGTCAACTGTGTACCCAGGGAACAGTGCACACAGATTTCATAGAGTGAACACGAGAGAAACAG
|||||
-AATGCCCAATTTGTATGGTGATANAAGTCCCGT
510 520 530 540
      1140 1150
GAAAAATCAAGACT

```

70. US-09-030-606-174 (1-1459)

US-09-020-747-10 Sequence 105, Application US/09020747

Initial Score = 43 Optimized Score = 193 Significance = 0.12
 Residue Identity = 40% Matches = 218 Mismatches = 305
 Gaps = 22 Conservative Substitutions = 0

```

      880 890 900 910 920 930 940
CATAAATAGTCGATTTATGCATACGTTTATGCTATCATGATATACCTTTGTGGAATTTTGTGATTTCT
|||||
      950 960 970 980 990 1000 1010
AAGGTACACAGTCTGCTGTGCAATTTTAAATTTGTGCAACTCTCCATAAATTTTCTGATGTGTTATT
|||||
ANTCAGACATATATTTATTTATATTTAAATTCATAGAAAAGTCCCTTACATTTAATAAAGTTTCTTTC

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      1020 1030 1040 1050 1060 1070 1080 1090
GAAAAATCCCAAGTATAAGTGGACTTTGTGCATTTCAAAACAGGGTTGTTCAAGGGTCAACTGTGTACCCAGAG
|||||
TCAAGTATCAGAGGATTTAGATATGCTTTTGAACACCAATATTAATTTGAGGAAATACACCAAAATACAT
100 110 120 130 140 150 160
      1100 1110 1120 1130 1140 1150
GGAACATGTGACACAGATTTATAGAGTGAACACGAAAGAGAAA-----CAGGAAAAATCAAGACT
|||||
TATCTAAATTTTAAAGATCATAGAGCTTTGAAGTGAAGAGATAAATTTGACCTCAGAAACTCTGAGCAAT
170 180 190 200 210 220 230
      1160 1170 1180 1190 1200 1210 1220
CTAAAGAGGCTGGCGAGGCTGGCT--CATGCCCTGTATCCAGCACTTTGGGAGGCGGAGCGAGCAGATC
|||||
AAATATCCACTATTAGCAATAAATTTACTATGGACTTCTCTCTTTTAAATTTCTGATGAATATGGGTCTCAG
240 250 260 270 280 290 300 310
      1230 1240 1250 1260 1270 1280 1290
ACTTGAGTAAAGGCTTCAAGACCCAGCCTGGCCAAATGGTGAATCTCTGTCTGTACTTAAATAACAAAAGT
|||||
TGGTAAACCAACACACTTCTGAAGGATACATTACTTTAGTGATAGATTTCTTATGTACTTTGCTTAATACGTGGAT
320 330 340 350 360 370 380
      1300 1310 1320 1330 1340 1350 1360
TAGCTGATATGTTGGCGAGGCGCTGTATCCAGCTACTTTGGGAGGCTGAGCGAGAGAAATTTGTTGAATA
|||||
-----ATGAGTTGACAAAGTTTCTCTTTTCAATCTTTTAAAGGCGCGAGAAATGAGGAGAAAGAAAG
390 400 410 420 430 440
      1370 1380 1390 1400 1410 1420 1430
TGGGAGGCGAGGTTGAAGTGAAGTTGA--GATCACACCACTATATCTCCAGCTGGGCGCAACAGAGTAAGACTC
|||||
GATTACGCATCTGTCTTCTATGGAAGGATTAGATATGTTTCTCTTTGCCAATATTAAATAAATAAATATG
450 460 470 480 490 500 510
      1440 1450 X
TGCTCTCAAAAAAATAAAAAA
|||||
TTTACTACTAGTGAACCC
520 530 X

```


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TCCCCGTCACACAGTAGGGTAATTTCTAGTCAGGTTTTTGGGGAGTCAAAAGTTATAAGAGGATTTTCTATTGG
|| |||| | - - -
TCTGTCTCAAAAAAAAAAAAAA
1440 1450 X

CAGAAACGAGCGCAAGAGTCCGCCGGGTAGGCCTGCGAAGCAAATGCTGATGCTCCGGATGSGTGTCAGACT
|| || | ||
ATTAAATTCGGTTGGCATCAGCCCGCTTTCNTTTCNGSAAACTGCTNCCCCTGCTNNTNNTGAATCGGGCCA
580 590 600 610 620 630 640 650

7500 7600 7700 7800 7900 8000 8100 8200 8300

TCTACTCTCTCTAGGACTGGGCTGATGAAGGACATGCCAAAAATTTCCCTATCCGCCAACTTTNCCCTACCC
 160 170 180 190 200 210 220
 920 930 940 950 960 X 970 980
 CTTGACTGCGCTGCCCTCCCTTTCCCTCTCTCAGTTGAGGAGTCCCTCTGGTCTTGCCTCCGCCGGC
 990 1000
 CGAACTTCCCCACCAGCTCCACAACCCCTTTTGGAGCTACTGCAGGT
 230 240 250 260 270 X
 GCAGAACATGNTGGGGTGGTACAGCG

10. US-09-030-606-174' (1-1459)
US-09-525-397-11 Sequence 11. Application US/09525397

Initial Score	=	64	Optimized Score	=	99	Significance	=	2.05
Residue Identity	=	40%	Matches	=	117	Mismatches	=	155
Gaps	=		Conservative Substitutions	=	14		=	0

630 640 650 660 670 680 690
 AGGTTTGGGAGTCAAAAGTTATTAAGAGGATTTCTATTGGTGGAGGTCACGGCCCTCAGGCCCCCATGC
 |
 AAATTCTACTCATCCCAATGA
 x 10 20

[illegible]

780
CTTTCCTCTCTTAATCCCTGTTATTATTCCTCTCAGTTCTCTCTAGTAGTCTCACTGCTGCC
790
||||| || | | | | | | | | | | | | | | | |
800
ACGGCTTCCCTAACCAACCCTCT---TCTCTTGCGCCAGCCTGGTCCCCCAC-----TTCCACTCCCC
810
||| | | | | | | | | | | | | | | | | | |
820
830
840

850 855 860 865 870 875 880 885 890 895 900 905 910
 CTGTGTCTCTCCATCTCTGCATCTCGCATCGCGCCTGTGTCTGTCTGTCTGCCCTTCTCCACGCTTC
 TCTACTCTCTCTAGACTGGGCTGATGAGGCACCTGCCCAAAATTTCCCTACCCCGCAACTTTCCTTACCC
 160 170 180 190 200 210 220
 CCTGAGTGCCTGCGCCTCCCTTTCCTCTCTCAGCTTCAGAGTTCCTTGGTCTTGCCTTCGCGCGC
 CCAACTTTCCCAACCACTGCTCCACAACTCTTTGGAGCTACTCAGGT
 230 240 250 260 X

990 1000 1010
GCAGAACATGNTGGGGTGGTACAGCG

11. US-09-030-606-174' (1-1459)
US-09-841-894A-1 Sequence 11, Application US/09841894A

Initial Score	=	64	Optimized Score	=	99	Significance	=	2.05
Residue Identity	=	40%	Matches	=	117	Mismatches	=	155
Gaps	=		Conservative Substitutions	=	14		=	0

630 640 650 660 670 680 690
AGGTTTTGGGGAGTCAAAGATTATAGAGGATTTTCATTGGTGGAGGTCACCGCCCTCAGGCCCATGC
AAATTCTACTCATCCCAATGA

TGTTGGAGGTCAACTGCATTCTATGTCTGTGTGTTCGCCCTCCCAATGCTGTCTTCTGTCTCTCTC
| | | | | | | | | | | | | | | | | | | | | |
T-----AATCCCAATGCTTGTAATCCCAAGGTTAGGGTCTTAGGAAGGTAGAGGGTGGGGGCTTCAGGTCTC

[illegible]

12. US-09-030-606-174' (1-1459)
US-08-904-809-66 Sequence 66, Application US/08904809

Initial Score	=	64	Optimized Score	=	108	Significance	=	2.05
Residue Identity	=	38%	Matches	=	123	Mismatches	=	182
Gaps	=		Conservative Substitutions	=	18		=	0

210 220 230 240 250 260 270
GGCAGGCGTGGTCTTGAACCTCTTACCTCAAGTGAATCGCTGCCCTCCCAAGTCTGGGATACAG
ACGCGTTTCCCTCAGAATTCAG
X 10 20

GCATGACCACTTCCGCCCTCTTTGTAGACTTGATTTTTCTGTTCCTCGTTCCACCTCAT
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
GGAGAGACACTCGCCTGCCTTCTCGTGTGTGCGTAGACCCTGTGTGCCCTT-----CCACACA
 50 60 70 80

[illegible]

ACAGACGAACGTGCTAGCTTAGAATAATCAAAAATCCACAAGGTATATCATGATGCATTAACCGTATT
| | | | | | | | | | | | | | | | | | | | | |
GCCCTGAATTTATGCTGGTTTTATATATTTTTAAAGAATGCACCTTTATGTCATTTTTTAATAAGTCTCGA

GCATAAATCGACTATTATTGTTATTTGTAAGGTCGCCGTCACAGTAGCATTATTCTAGTCA
AGAAATTACTGTTT
300 X

13. US-09-030-606-174' (1-1459)
US-09-020-747-66 Sequence 66, Application US/09020747

Initial score	=	64	Optimized score	=	108	Significance	=	2.05
Residue identity	=	38%	Matches	=	123	Mismatches	=	182
Gaps	=		Conservative substitutions	=	18		=	0

[illegible]

Initial Score	=	62	Optimized Score	=	248	Significance	=	1.92
Residue Identity	=	35%	Matches	=	278	Mismatches	=	492
Gaps	=		Conservative Substitutions	=	11		=	0

19. US-09-030-606-174' (1-1459)

[illegible]

24. US-09-030-606-174' (1-1459)
US-09-071-710-16 sequence 16, Application US/09071710

Initial Score	=	62	Optimized Score	=	307	Significance	=	1.92
Residue Identity	=	38%	Matches	=	349	Mismatches	=	591
Gaps	=		Conservative Substitutions	=	35		=	0

[illegible]

AGCTTANTGCAGACCTCNTCAGACACACCGCAGCGTTTCACGCACTGCAGCACGGTAGGCAATTCGCTCGG
 TGTCTCCGTACGTCGTGGTGGGTGAGCCACCGAGCGCAGGGTGGTTCCGGGCCGAGGCATCTGCTCGGA
 510 520 530 540 550 560 570

ACGCGAGAGCTCTGGGTGAGCCCGCGGACTGGGCAGAGGACCTCTTGAAGAGGCGACACACACCGGTGA
 CCTCCCATCTGTGATAGTGCCTTCCTGTGTCCAGGTGGCCCATCCCTGTTTATGGGTCCCAATTGTCCA
 580 590 600 610 620 630 640 650

1170 1180 1190 1200 1210 1220
 GGTCA-----CCGTGCGCAGCAGACCCAGCAGAAAGAGGCAAGAGTTCCCGCGGTAGGGCACT
 GCTCAGCAGTCTGTCACTGCGCTATATGTGTCTGCGCAGAGGCTGGGTCTGTGCGCCATTACTTTGCTTAC
 660 670 680 690 700 710 720

1230 1240 1250 1260 1270 1280 1290
 GC--GAAGCAATGCTGATGCTCCGGATGGTGTGAGACTCGGACACCGGATTCGTCCAACTGATGAGCATGAG
 ACAGTAGTATTGTGACAAGACGCACTTGGCCAAATACTCAGCGTAGAAAATTCACAGACATTTGGGTGGGAG
 730 740 750 760 770 780 790

1300 1310 1320 1330 1340 1350 1360 1370
 GTCTGTAGCGACGAAGGTCTGTGTACTCTGGTGCCGTACGGAGAGCTGGCTCCACCATCTGGCTCC
 GGCTCGCTCACTGGGTCCAGCTCCCGCTCTCTGTAGCCCATGGGCTGCGGGGTGCGCCGCCAGCTTC
 800 810 820 830 840 850 860

1380 1390 1400 1410 1420 1430 1440
 TGCTCTTGGTCGGCTCAAGACTGTGAGGCCCGGATGGTGTAGGAGCTGTGCACTCACTTCATCTCGGA
 TGTGTGTCGCAAGTAATGTGCTCTCTGCTGCCACCCCTGTGTGCTGAGTCCGTAGCTGCACACCTGGG
 870 880 890 900 910 920 930 940

1450
 ACAGTGTGGCGGTGACC
 GCTGGGGGCTCCCTCTCTCTCTCTCCCCAGTCTCTAGGGCTGCCTGACTGGAGGCCCTTCCAAAGGGGT
 950 960 970 980 990 1000

25. US-09-030-606-174' (1-1459)

25. US-09-030-606-1/4, (1-1459)
US-09-525-397-16 sequence 16, Application US/09525397

Initial Score	=	62	Optimized Score	=	307	Significance	=	1.92
Residue Identity	=	35%	Matches	=	349	Mismatches	=	591
Gaps	=		Conservative Substitutions	=	35		=	0

[illegible]


```

27.  US-09-030-606-174' (1-1459)
      US-08-850-713-16 Sequence 16, Application US/08850713

      Initial Score = 62 Optimized Score = 308 Significance = 1.92
      Residue Identity = 35% Matches = 350 Mismatches = 590
      Gaps = 33 Conservative Substitutions = 0

      ATCAGAAAAATTTTAGAGAGTTCACACATTTAAAAAATTCACACACGCACTGTGTAGCTTAGAAGATATC
      460 470 480 490 500 510 520
      |||||
      GGGGCTGTACCGGGCGTCCCC
      x 10 20

      530 540 550 560 570 580 590
      AAAAATTCACAAAGGTATATCATGATCAATAAAGTATGCAT---AAATCGACTATTATTATTGTTATTG
      |||||
      AGAGCTGACCGCGGCACCGAGGCGCGGACACTATGATGAAGGCTTCGATGGCGAGCTGGGCGCTGTTTC
      30 40 50 60 70 80 90

      600 610 620 630 640 650 660
      GTAAGCTCCCGTCACAGCTAGGCTATTCTTAGTCAGGTTTTTGGGAGGTCAAAAGTT--ATAAGAGGATT
      |||||
      TATGACCAAGGCTGCTGCTGATGACATCGGACCGGATTCGGCACTCGAGCA
  
```

[illegible][illegible]

[illegible][illegible]

Initial Score	=	55	Optimized Score	=	166	Significance	=	1.44
Residue Identity	=	36%	Matches	=	172	Mismatches	=	295
Gaps	=	6	Conservative Substitutions	=	0			

[illegible]

700	900	910	920	930	940
-----	-----	-----	-----	-----	-----

750 800 810 820 830 840
CCGTGTTATTCTCTGTTCTCTCAGTTTCTCTCTAGTTGTCACGTCT

TTTTCTTCANTNT
750 X

42. US-09-030-606-174' (1-1459)
US-09-020-747-40 Sequence 40, Application US/09020747

Initial Score =	53	Optimized Score =	232	Significance =	1.35
Residue Identity =	3%	Matches =	256	Mismatches =	493
Gaps =	20	Conservative Substitutions	=	-	0

42.	US-09-030-606-174' (1-1459)				
	US-09-020-747-40	Sequence 40,	Application US/09020747		
	Initial Score	=	53	Optimized Score	= 232
	Residue Identity	=	3%	Matches	= 256
	Gaps	=	20	Conservative Substitutions	= 0
				Mismatches	= 493
				Significance	= 1.35

Gaps = 20 Conservative Substitutions

	10	20	30	40	50	60	70
TTTTTTTTTTTTTTTTTTGAGACAGAGCTACTCTCTGCCCCAGCTGAGGATATAGTGGTGATCATCAAC							
				GTGGTATTTTCTGTAAAGATCAAGGTGTTCTCTCCCTCG			
				x	10	20	30

Gaps

17 Conservative Substitutions

○
11
—

550 560 570 580 590 600 610
ATGAATGCATAAACCTATGCATAAATCGACTATTATGTTATGGTAAGCTCCCGCTCAACAGTAGGCTA
GCCTTTCTCTCCCTCCTCTG
X 10 20

620
TTTCTAGTCAGGTTTTGGGAGTCAAAATTATAGAGGATTTTCTATTGGGTGGAGTGCACGGCCCTCAG
AATTTAACTTTTCAACTTGC AATTTGCAAGGATACACATTTCACTGTGATATTTGTGTTGC AAAAA
30 40 50 60 70 80 90

GCCCCATGCTGTGGGAAGGCACACTCATTTCTATGTGTGTGCTTTCGCTCCCATCCTGTTTCGTT
| | | | |
AAAAAGTGCTTGTGTAAATACTTGTGTGTGAATCCATCTTGCTTTTTCCCATT-----TG

[illegible]

ACTGTCCTCCGTGTGTCCTCGCATCTCGGCCTGTGTGTCTGTCTGCCCTTCT
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
ACAGTGTAATGGATGGTGTCT-CAGAACCAATTTCACCCAGACAGCCTGTTCATCTCTGTTTAATAATTAG
230 240 250 260 270 280 290

[illegible]

C
X

US-09-030-606-174' (1-1459)

[illegible]

ATGAGCCACCCGCGCCAGCCCTTGTGAGAGCTGTGATTTTCTGCTTCCTGCTGCTGTTTCCACCTCTATGA
|||||
ACCTTTTATTTAAATGTTTATA
x 10 20

[illegible]

TAGTAATTTACCAATTAACACAGTTTAAAAAGAGATAATATATTCACAGCANNTACAAATATCTATATGAAGA
 100 110 120 130 140 150 160
 CACACCAACCTCTACCTTGGAAATATCAAAAAATTCACACAAAGGTATATCATGTAATGATCAATAAAGCGTATG
 500 510 520 530 540 550 560

[illegible]

TCACTTCAACCTCTGCCTCCCATATTCAGCAATTCTCCTCAGCTCCCAAGTAGCTGGGATTACAGG
| | | | | | | | | | | | | | | |
TAGGTTTAGAGGAACCCCTCATAGATGAAACCCCCCGAGACGACACTGCACTGCCAAGCACGCCG

CGCCCTGCCACCATCCAGCTACTTTTGTATTTTATACAGACAGATTTCACCAATTTGGCCAGGCTGG
GGGTAGGAGGGGGCCCTATGCACAGCTGGGCCCTTGACAGACAGGCGCTTCGA-----TGTCAAGCTCGA

TCTTGAACTCGTTACCTCAAGTGATCTGCCTGCCCTCCCAAGTCTGGGATTACAGGATCAGGCAC
 230 240 250 260 270 280
 TGTCAATGTTCTGTAAGCGGGCGGTGTACCTGGGTAGGGGCACACCGTACGGGGCCACCAAGAACCTTCAA
 180 190 200 210 220 230 240 250 260 270 280 290 300

[illegible][illegible]

CTGCGACTTCTCTCNAANA-----CATGATGTTGGGCTCNAACCCACCCACANNCGGACTTCCCTTGANG
 390 400 510 520 530 540 550 560 570
 AACTGTGCTAGCTTTAGAAATATCAAAAAATCCCAAGAAGTATATCATGAATGCATAAAGCTATGCATATAA

GAATCCCAAATCTCTTCGNTCTTGGGCTTCTNCTGATGCCCTTANCTGGTTGCCCGNGATGCCAANCANCC
520 510 500 490 480 470 460

TCGACTATTATTCTTATTCGTAAAGCTCCCGCTCAACAGTAGGCTATTCTAGTCAGGTTTTGGGAGTCA
640 630 620 610 600 590 580

CAANCCCGGGTCTCTAAANACACCCNCCTCCTCTTTTCATCTGGTGTNTNTCCCGGACCGTGTGTTCCCTCT
530 540 550 560 570 580 590
AAAGTTATAAGAGGATTTTCTATTGGGTGGAGGTACCGGCCCTCAGGCCCATGCTGTGTGGAGGTCAACTG
650 660 670 680 690 700 710

CAAGGGAGCCCATATCTCACCANTACTCACCTNCCGCCCTGNNACCACCTCTTANNNGNTCCCGC
600 610 620 630 640 650 660

790 800 810 820 830 840 850
CCTGTTTATTTCTCTGTGTTCTCTCAGTTTCTCTCTACTGTCTCCCTGTGT
|||||
TTTTTTTTCCTCAATTNT

750 X

3. US-09-030-606-174' (1-1459)
US-09-020-747-11 Sequence 115, Application US/09020747

```

Initial score = 32 Optimized score = 99
Residue identity = 36% Matches = 141 Mismatches = 225

```


[illegible]

45. US-09-030-606-174' (1-1459)

US-09-020-747-46 Sequence 46, Application US/09020747

Initial Score	-	52	Optimized Score	-	198	Significance	=	1.28
Residue Identity	-	34%	Matches	=	207	Mismatches	=	382
Gaps	-	3	Conservative Substitutions	=	0		=	0

[illegible]

640	650	660	670	680	690	700	710
GAGTCAAAAGTTTAAAGAGGATTTTCTATTGGGTGGAGGTACACGCCCTCAGCGCCCATGCTGTTGGAGGT							
AAC TGAAGGCGCANAAGAAATTAATTTTCAC T CATGTAAACNCACCCANATTTACAATGCTTAATGCGANGG							
320	330	340	350	360	370	380	
CAACTGCATTTCTATGTCTGTGTGTTTCTGCCTCCCATCTCTGTTTCTGTTTCTCTCTCTCTTCTGCTTCTCTC							
AAAMAGCACTGGAAGTAGGGAAGTANTCAAGGCTTTTCTGGTCTCTAACTGCGCTTACTCTCTTGGGTGTCGC							
390	400	410	420	430	440	450	
790	800	810	820	830	840	850	
TTTATTCCTGCTGTTTATTTCTCTCTGTTTCTCTCAGTTTCTCTCTAGTTGTCTAGTGTCTCCCTGTGTCTCTC							
TTTGA TCCCTCTGGAGACAGCTGCCAGGCTCTCTGTATATCCACAA--TCCCAGCAGCAAGATGAAGGATG							
460	470	480	490	500	510	520	
860	870	880	890	900	910	X	
TCATCTCTGCATCTCGCCATCGGGCCCTGTGTCTCTCTCTCCCTCTCTCCACCCCTTCCCTGAGTCGCC							
AAAAAGGACACATGCTGCTTCTCCCTTTGGAGGAGCTTTCATCTCACTGCGCCAAACACTCAGTCACATCT							
530	540	550	560	570	580	590	
930	940	950	960	970			
TGCGCTTCCCTTTTCCCTCTCTCAGTTTGGAGGAGTCTTCTCGG							

46. US-09-030-606-174' (1-1459)

#0: US-03-030-000-174 (1-1435)
US-08-806-596-16 Sequence 16, Application US/08806596

Initial Score	=	52	Optimized Score	=	257	Significance	=	1.28
Residue Identity	=	35%	Matches	=	284	Mismatches	=	498
Gaps	=	15	Conservative Substitutions	=	0			

[illegible]

390 400 410 420 430 440 450 460
 CCTTGACACCCCTGGTTGCAATGCACAGTCACCTATACTTTGGATTCTTCAATTAACACATACAGAAAA
 -----AATTGTGGAACACACTCTATTGGCTACT---ATTTAAGAAAATACCAAAATCTTTC

GTGGTGTCTGAGGAGCTTCGAGTAAGCTCTATGACCCGCTGTACCCAGCATGTTCTGGCGCCGGCGGA
450 460 470 480 490 500 510

TAGAAATATCAAAAATTCCACAAGGTATATCA-TGAATGCATATAAAGSTATGTCATAAAATCGACATATT
| | | | | | | | | | | | | | | | | | | | |
GTGGTGCTCAGAGAGTCTGCAAGTAAGTCTCTCACCGCTGTACCACCCCAGCATGTTCTCGCGCGCGG

Thu May 1 15:12:23 2003

[illegible]

IntelliGenetics

FastDB - Fast Pairwise Comparison of Sequences Release 5.4

Results file us-09-030-606-175.res made by tport on Thu 1 May 103 15:04:43-PDT.

Query sequence being compared:US-09-030-606-175 (1-1167)
 Number of sequences searched: 410
 Number of scores above cutoff: 410

Results of the initial comparison of US-09-030-606-175 (1-1167) with:

```
File : 6130043.seq
File : 6252047.seq
File : US08806596.seq
File : US08850713.seq
File : US08904809.seq
File : US09020747.seq
File : US09841894A.seq
```

1000-

Z

Z

Z

Z

Z

Z

Z

Z

Z

Z

Z

Z

Z

Z

Z

Z

Z

Z

Z

Z

Z

Similarity matrix
Mismatch penalty
Gap penalty
Gap size penalty
Cutoff score
Randomization group

Similarity matrix	Unitary	k-tuple
Mismatch penalty	1	Joining penalty
Gap penalty	5.00	Window size

Similarity matrix	Unitary	k-tuple	4
Mismatch penalty	.	Joining penalty	30

1992

12-4-2010

Similarity matrix	Unitary	k-tuple	4
Mismatch penalty	.	Joining penalty	30

Similarity matrix	Unitary	k-tuple	4
Mismatch penalty	.	Joining penalty	30

Similarity matrix	Unitary	k-tuple	4
Mismatch penalty	.	Joining penalty	30

1. US-09-030-606-175 (1-1167)
US-09-020-747-17 Sequence 175, Application US/09020747

Initial Score	-	1167	Optimized Score	-	1167	Significance	-	18.54
Residue Identity	-	100%	Matches	-	1167	Mismatches	-	0
Gaps	-	0	Conservative Substitutions	-	0		-	0

X 10 20 30 40 50 60 70
 GCAGCCCTGGCAGCGCACTGTCATGAAACGAATTTCTGCTCGGCGTCTCGTGCATCCGAG
 GCAGCCCTGGCAGCGCACTGTCATGAAACGAATTTCTGCTCGGCGTCTCGTGCATCCGAG
 X 10 20 30 40 50 60 70

80 90 100 110 120 130 140
TGGGTGCTGTCACCCGCACACTGTTTCCAGAACTCCTACACATCGGGCTGGGCCTGCACAGTCTTGAGGCC
TGGGTGCTGTCACCCGCACACTGTTTCCAGAACTCCTACACATCGGGCTGGGCCTGCACAGTCTTGAGGCC

150	160	170	180	190	200	210	
GACCAAGACCAGGAGCAGATGGTGGAGCCAGCCTCTCCGTACGGCACCCAGAGTACAAAGACTCTTG							
155	165	175	185	195	205	215	
GACCAAGACCAGGAGCAGATGGTGGAGCCAGCCTCTCCGTACGGCACCCAGAGTACAAAGACTCTTG							
160	170	180	190	200	210		
220	230	240	250	260	270	280	
CTCGCTTAACGACTCATGCTCATCAAGTTGGAGCAATCCGTGTCCAGTCTGACACCATCCGGAGCATCAGC							
225	235	245	255	265	275	285	
CTCGCTTAACGACTCATGCTCATCAAGTTGGAGCAATCCGTGTCCAGTCTGACACCATCCGGAGCATCAGC							
230	240	250	260	270	280		
290	300	310	320	330	340	350	360
ATTGCTTCGAGTGGCCCTACCGCGGGGAACTCTTGCCTGNTCTGCCTGGGCTCTGTGCGCAACGGCAGA							
295	305	315	325	335	345	355	365
ATTGCTTCGAGTGGCCCTACCGCGGGGAACTCTTGCCTGNTCTGCCTGGGCTCTGTGCGCAACGGCAGA							
300	310	320	330	340	350		
370	380	390	400	410	420	430	
ATGCCTAACGCTGTGCACGTGCGTGAACCTGCGGTGTCTGAGGANTCTGCAGTAACTCTATGACCGG							
375	385	395	405	415	425	435	
ATGCCTAACGCTGTGCACGTGCGTGAACCTGCGGTGTCTGAGGANTCTGCAGTAACTCTATGACCGG							
380	390	400	410	420	430		
440	450	460	470	480	490	500	
CTGTACCACCCCAGCATGTTCTGCGCGCGGAGGGCAAGACCAAGAGGACTCCTCGACCGTGACTCTGGG							
445	455	465	475	485	495	505	
CTGTACCACCCCAGCATGTTCTGCGCGCGGAGGGCAAGACCAAGAGGACTCCTCGACCGTGACTCTGGG							
450	460	470	480	490	500		
510	520	530	540	550	560	570	
GGGGCCCTGTATCTGCAACGGGTACTTGCAGGGCCCTGTGCTTTTCGGAAAGCCCGCTGTGGCCAACTTGGC							
515	525	535	545	555	565	575	
GGGGCCCTGTATCTGCAACGGGTACTTGCAGGGCCCTGTGCTTTTCGGAAAGCCCGCTGTGGCCAACTTGGC							
520	530	540	550	560	570		
580	590	600	610	620	630	640	
GTGCCAGGTGTCTACCAACCTCTCAAAATTCACCTGAGTGTGATAGAAAACCGTCCAGNCAGTTAACTC							
585	595	605	615	625	635	645	
GTGCCAGGTGTCTACCAACCTCTCAAAATTCACCTGAGTGTGATAGAAAACCGTCCAGNCAGTTAACTC							
590	600	610	620	630	640		
650	660	670	680	690	700	710	720
TGGGACGTGGAAACCATGAAATTCACCCCAAAATCATCTCTGCGGAANGAATTCAGGAATATCTGTTCCCA							
655	665	675	685	695	705	715	725
TGGGACGTGGAAACCATGAAATTCACCCCAAAATCATCTCTGCGGAANGAATTCAGGAATATCTGTTCCCA							
660	670	680	690	700	710	720	
730	740	750	760	770	780	790	
GGCCCTCTCCCTCAGGCCCAGGAGTCCAGGCCCCAGGCCCTCTCCCTCAAAACCAAGGTTACAGATCCCC							
735	745	755	765	775	785	795	
GGCCCTCTCCCTCAGGCCCAGGAGTCCAGGCCCCAGGCCCTCTCCCTCAAAACCAAGGTTACAGATCCCC							
740	750	760	770	780	790		
800	810	820	830	840	850	860	
AGCCCTCTCCCTCAGGCCCAGGAGTCCAGGCCCCAGGCCCTCTCCCTCAAAACCAAGGTTACAGATCCCC							
805	815	825	835	845	855	865	
AGCCCTCTCCCTCAGGCCCAGGAGTCCAGGCCCCAGGCCCTCTCCCTCAAAACCAAGGTTACAGATCCCC							
810	820	830	840	850	860		
870	880	890	900	910	920	930	
CTCCTCCNTCAGACGCGAGGTCCAGACCCCGCCAGCCCTCTCCCTCAGGCCCTCTCCCTCAAAACCAAGGTTACAGATCCCC							
875	885	895	905	915	925	935	
CTCCTCCNTCAGACGCGAGGTCCAGACCCCGCCAGCCCTCTCCCTCAGGCCCTCTCCCTCAAAACCAAGGTTACAGATCCCC							
880	890	900	910	920	930		
940	950	960	970	980	990	1000	
CCCTCTCCNTCAGACGCGAGGTCCAGACCCCGCCAGCCCTCTCCCTCAGGCCCTCTCCCTCAAAACCAAGGTTACAGATCCCC							
945	955	965	975	985	995	1005	
CCCTCTCCNTCAGACGCGAGGTCCAGACCCCGCCAGCCCTCTCCCTCAGGCCCTCTCCCTCAAAACCAAGGTTACAGATCCCC							

[illegible]

GGTGTGCTCAGCAGNCTCGTAGTCTCTATGACCGCTGTACACCCAGCATCTTCGTGGCGGGGG
400 410 420 430 440 450 460
CCAGCAAGCTCAGGAGTGTTCACCATTTGTGTGTACCCAGGGACCCAGCAGCTGCAACTCAGCAA
310 320 330 340 350 360 370

520 530 540 550 560 570 580
GCAACGGTACTTCGAGGGCTTGTTCTTCGGAAAGCCCGCTGGCCAACTTGGCGTGCCAGGTGTCCT
ANAGNCACCANACCGAGCTGTCCNANAAGCCTNNNATACNGNNNATCCCAATTGTGNANCCCTCCNAAGTAT

80 90 100 110 120 130 140 150
 CTGTCAGCGCGACACTGTTTCCAGAACTCTCTACACCATCGGGCTGGGCTGCAGACTCTTCAGCGCCGACCA
 160 170 180 190 200 210 220
 GAGCCAGGGAGCCAGATGTTGGAGCCAGCCTCTCCGTAGCGCACCCAGAGTACAAAGACTCTGTCTCGCT
 230 240 250 260 270 280 290
 AACGACCTCATGCTCATC-AAGTTGGACGAATCCGGTGTCCGAGTCTGACACCATCCGGAGCATCAGCATTCG
 300 310 320 330 340 350 360
 TTCGACGTGCCCTACCGCGGGGAACTCTTGCCCTGNTCTCGGTGGGGTCTGCTGGCGAACGCGAATGCC
 370 380 390 400 410 420 430
 TACCGTGTGCACCTGCGTGAACCTGTGCGTGTCTGAGGAGTCTGCAGTAAGCTCTATGACCCGCTGTGA
 440 450 460 470 480 490 500
 CCACC--CCAGCATGTTCTG-CGCCGCGGAGGGCAAGACCAAGAGACTCTCTCAACGGTGACTCTGGGGG
 510 520 530 540 550 560 570
 GCGCTGATCTGCACAGGGTACTTGCAGGGCCTTGTTCTTCGAAAAGCCCGGTGCGCCAACTTGGCGT
 580 590 600 610 620 630 640
 GCCAGTGTTCTACACCAACCTCTGCAATTACTAGT---GGATAGAGAAACCGTCCAGNCACAGTAACT
 650 660 670 680 690 700 710
 CTGGGACTGGGAACCATGAAATTTGACCCCAATACATCTCTGCGGAANGAATTCAGGAATATCTGTTCC
 720 730 740 750 760 770 780 790
 AGCCCTCTCTCTAGGCCAGGAGTCCAGGCCCGCCCTCTCTCCCTCAACCAAGGGTACAGATCC
 800 810 820 830 840 850 860
 CAGCCCTCTCTCTCAGACCCAGGAGTCCAGACCCCGCCCTCTCCCTCAGACCCGAGGTCCAGCG
 870 880
 CCTCTCTCTCTCAGACGAGCAG

15. US-09-030-606-175 (1-1167)
US-09-020-747-84 Sequence 84, Application US/09020747

Initial Score	=	64	Optimized Score	=	115	Significance	=	0.48
Residue Identity	=	34%	Matches	=	113	Mismatches	=	213
Gaps	=	0	Conservative Substitutions	=			=	0

GTAGCCTATGGCGGTGCCACGGANGGGCTCTGTGAGGCACGGGACAGTCACTTCCAAAGTATCTCTCGCGCGCG
10 20 30 40 50 60 70 80 90
TGTTCTGGAAGAAACGAATTTGTTGCTCGGGCGTCTCTGGTGCATCCCGAGTGGTGCTGTTCAGCGGCACACT
30 40 50 60 70 80 90
TCTTCTACCGTCCCTACCTTGCAGATCTTCGGCGAGATTCCCGCAGGAGACATGGACGCTGGCCCTCATGGAGC
80 90 100 110 120 130 140
100 110 120 130 140 150 160
GTTTCCAGAACTCCTACACATCGGGCTGGGCTGCAGACTTTCAGGCGCACCAAGAGCGCAGGACCCAGA
150 160 170 180 190 200 210 220
ACAGCAACTGTCTGTCTGGAGCCCGGGTCTTGGGCACACCCCTCTGGGCGCAGGCGGCGCACTTCGCTCTCCC
170 180 190 200 210 220
TGTTGGAGCCAGCCTCTCCGTACGGCACGCCAGAGTACACAGACTCTTGTCTGCTAACGACCTCATGTCTCA
230 240 250 260 270 280 290 300 310
AGTATGCCAACTGCTGGTGTCTGCTCTCTGCTCATCTTCCTGCTGCGTGGCAACATCTCTCTGGTCACTT
230 240 250 260 270 280 290
240 250 260 270 280 290 300 310
TCAAGTTGGAGGAATCCGTTGCCAGTCTGACACCATCCGGAGCATCAGCATGCTTCGACGTGCCCTACCG
320 330 340 350 360 370
GCTCATTCGCATGTTTCAGTTACATCTTACATCTCGGCAAGTAGTACGGGCAACAGCAGNATCTTCTACTGGGAAGCCAGCG
300 310 320 330 340 350 360
CGGGAACCTTTGGCTCGTNTCTGCTGGGGTCTGTGCGGCAAGGCAGAAATGCCTTACCGTGTCTG
320 X 330 340 350 360 370
TTNCCGCCTCATCCGG
370 380

US-09-030-606-175 (1-1167)

[illegible]


```
CAAAAGACAGTGTGGGTGAGGGGACCTGGTTCCTGTGTGGTGGCCCTCAGGACTCTTCCCTACAAA
170 180 190 200 210 220 230
470 480 490 500 510 520 530
GGAGGACAGACCAAGAGACTCCTGCAACGCTGACTCTGGGGGCCCTGATCTGCAACGGGTACTTCAG
|||||
TAACTTTTATGTTTCAATCCCATGGAGGAGTGTTCATCTAGAACTCCATGCAAGAGCTACATTA-
240 250 260 270 280 290 300
540 550 560 570 580 590 600
GGCTTTGTCTTTTCGGAAGACCCCGTGTGGCCAACTTGGCGTCCAGGTCTCTACACCAACCTCTGCAA
-ACGAGCTGACAGTTAGGGCTTANAGATGGGAAACACAGGTGACTGAGTTATTCAGCTCCCAAAACCC
310 320 330 340 350 360 370 380
610 620 630 640 650 660 670
TTCACCTGAGTGATAGAGAAACCCCTCCAGNCCAGTTAACTCTGGGACTGGGAACCCATGAATTCACCC
|||||
TTCTCTAGTGTGT-CTCAACTPAGGAGGTAGCTGTTAAACCTGAGCCTGGGTAATCCACCTGCAGAGTCCC
390 400 410 420 430 440 450
680 690 700 710 720 730 740 750
CAAATACATCCTCGCGAANGAATTCAGGAATATCTGTTCCAGCCCTCTCCCTCAGGCCCAGGAGTCCAG
|||||
CGCATTCAGTGCATGGACCCCTCTGGCTCCCTGT-----ATAAGTCCAGACTGAACCCCTTG-GAAG
460 470 480 490 500 510
760 770 780 790 800 810 820
GCCCCAGCCCTCTCCTCAACACAGGTACAGATCCCGAGCCCTCTCCTCCTCAGACCCAGGAGTCCA
|||||
GNCTCACTGACGAGCCCTTANAACTGGGGAAGAAAGAAAGGAGCGCCCAACCCCACTGTGCA-----
520 530 540 550 560 570 580
830 840 850 860 870 880 890
GACCCCAAGCCCTCTCCTCAGACCCAGGAGTCCAGCCCTCTCCTCCTCAGACGAGGAGTCCAGACCC
-NCTAGGACCTCAGACGACAGGTTGGGAGCAAAAACCACTTACTTTGGCAC-----AAACAAAACT
590 600 610 620 630 640 650
900 910 920 930 940 950 960
CCGAGCCNTCCTCCTCAGACCCAGGAGTCCAGCCCGCCCAACCCCTCTCCTCCTCAGAGTTCAGAGTCCAAG
|||||
NGGGGGCAACCCCGGACCCCNANGGGGTTACAGCAANCGGNAACNTGGAACCAATTNAGGCGAG
660 670 680 690 700 710 720
970 980 990 1000 1010 1020 1030
CCCCCAACCCCTCTGTTCCAGACCCAGAGTTCAGGTCAGGCTCCCTCCTCAGACCCAGGAGTCCAA
|||||
CCCNCCACCCNAATNTGCTGGGAATTTTCTCCCTCAATTTTTC
730 740 750 760 770 780 790
1040 1050 1060
TGCCACCTAGANTNTCCCTGTACACAGT
```

17. US-09-030-606-175 (1-1167)

US-08-904-809-23 Sequence 23, Application US/08904809

Initial Score = 61 Optimized Score = 252 Significance = 0.43
Residue Identity = 33% Matches = 298 Mismatches = 559
Gaps = 37 Conservative Substitutions = 0

```
150 160 170 180 190 200 210 220
AAGAGCCAGGAGCCAGATGGTGGAGGCCAGCCTCTCCAGGACCCAGAGTACAACAGATCTTGTCTCG
|||||
CTAAGACCTCATGCTCATCAAGTGGAGAAATCGGTGCCAGTCTGACACCATCCCGAGCATCAGCATTG
|||||
ACTGTGCGCCTCGCTNCTCTTTTCTCCCGCAACCATGTCTGA--CNANCCGATTTGGCNGATATCNAAA
30 40 50 60 70 80 90
GCACAACTATACTTCGCTCGN
X 10 20
```


270
 GACACCATCGGAGCATCATCTTCGCAGTGGCCCTACCCGCCGGGAACCTTGCC--TCGTNTCTGG-
 -----ACATCATCAACCACTTAAGCCTGCCCANAAACCCAACTTCAGCGCATTTCTTACCAAAGAAGAAAGG
 300 310 320 330
 50 60 70 80 90

x 10 20
GCGCAGCCCTGGCAGGCGGCAC

[illegible][illegible]

30	40	50	60	70	80	90
TGGTCATGAAAACGAATCTGCTCGGGGCTCTGTGTCATCCGAGTGGGTGTGTAGCCGCACACT						
TGGTTCGGGCGGGGCATCTGCTCGAACCTCGCATCTCGATAGTCCCTCTCTGCTGCCAGTGGGCC						
550	560	570	580	590	600	610
100	110	120	130	140	150	160
GTTTCCAGAACTCCTACACCATCGGGCTGGCCCTGCACAGTCTTGAGGCGCACCAAGAG----CCAGGGAGCC						
CATCCCTGTTTATGGGCTCCATGTCTCCAGCTCAGCCAGTCTGTCTCACTGCCTATATGTTGTCTGCCGAGGCC						
620	630	640	650	660	670	680
170	180	190	200	210	220	230
AGATGTTGGAGGCCAGCGCTCTCCGCTAGCGCACCCAGAGTACACAGACTCTTGTCTCGCTACGACCTCATGC						
TGGTCTGTCGCCATTTTACCTTTTCTACACAGGTAGTATTGTGACAAAGACGCACTTGGCCAAATACTCAGCGT						
690	700	710	720	730	740	750
240	250	260	270	280	290	
TCATCAAGTTGACGAATCCGTGTCGAGTCTGACACCATCCGGAGCATCAGCATGTCT-----TCGCA						
AGAAACTTCCAGCACATTTGGGGTGGAGGCGCTGCCCTCACTGGGTCCCAAGTCCCGGCTCTCTGTTAGCCCCA						
760	770	780	790	800	810	820
300	310	320	330	340	350	360
GTGCCCTACCGGGGGAACCTCTTGCTCGTTCCTGCTGGGTCTGCTGGCAACGGCAGAAATGCTACCGT						
TGGGGCTGTCGGGGCTGGCGCGCAGTTTCTGTTGTCGCAAGTAATGTGGTCTCTCTGCTGCCACCTCTGTCT						
840	850	860	870	880	890	900

CGTCCGCTACGCTGCACAGTCGGGGGTGGGCGTCCCTCTCTCTCTCTCCCCACTCTCTAGGGGTGCCT

G-----TACCACCCGAGCATGTTCTGGCCCGGAGGGCAAGACCAGAAGACTCTCTGCACCGTGACTC

[illegible]

[illegible]

270	280	290	300	310	320	330	340	350	360	370	380	390	400	410	420	430	440	450	460	470	480	490	500	510	520	530	540	550	560	570	580	590	600	610	620	630	640	650	660	670	680	690	700	710	720	730	740	750	760	770	780	790	800	810	820	830	840	850	860	870	880	890	900	910	920	930	940	950	960	970	980	990	1000	1010	1020	1030	1040	1050	1060	1070	1080	1090	1100	1110	1120	1130	1140	1150	1160	1170	1180	1190	1200	1210	1220	1230	1240	1250	1260	1270	1280	1290	1300	1310	1320	1330	1340	1350	1360	1370	1380	1390	1400	1410	1420	1430	1440	1450	1460	1470	1480	1490	1500	1510	1520	1530	1540	1550	1560	1570	1580	1590	1600	1610	1620	1630	1640	1650	1660	1670	1680	1690	1700	1710	1720	1730	1740	1750	1760	1770	1780	1790	1800	1810	1820	1830	1840	1850	1860	1870	1880	1890	1900	1910	1920	1930	1940	1950	1960	1970	1980	1990	2000	2010	2020	2030	2040	2050	2060	2070	2080	2090	2100	2110	2120	2130	2140	2150	2160	2170	2180	2190	2200	2210	2220	2230	2240	2250	2260	2270	2280	2290	2300	2310	2320	2330	2340	2350	2360	2370	2380	2390	2400	2410	2420	2430	2440	2450	2460	2470	2480	2490	2500	2510	2520	2530	2540	2550	2560	2570	2580	2590	2600	2610	2620	2630	2640	2650	2660	2670	2680	2690	2700	2710	2720	2730	2740	2750	2760	2770	2780	2790	2800	2810	2820	2830	2840	2850	2860	2870	2880	2890	2900	2910	2920	2930	2940	2950	2960	2970	2980	2990	3000	3010	3020	3030	3040	3050	3060	3070	3080	3090	3100	3110	3120	3130	3140	3150	3160	3170	3180	3190	3200	3210	3220	3230	3240	3250	3260	3270	3280	3290	3300	3310	3320	3330	3340	3350	3360	3370	3380	3390	3400	3410	3420	3430	3440	3450	3460	3470	3480	3490	3500	3510	3520	3530	3540	3550	3560	3570	3580	3590	3600	3610	3620	3630	3640	3650	3660	3670	3680	3690	3700	3710	3720	3730	3740	3750	3760	3770	3780	3790	3800	3810	3820	3830	3840	3850	3860	3870	3880	3890	3900	3910	3920	3930	3940	3950	3960	3970	3980	3990	4000	4010	4020	4030	4040	4050	4060	4070	4080	4090	4100	4110	4120	4130	4140	4150	4160	4170	4180	4190	4200	4210	4220	4230	4240	4250	4260	4270	4280	4290	4300	4310	4320	4330	4340	4350	4360	4370	4380	4390	4400	4410	4420	4430	4440	4450	4460	4470	4480	4490	4500	4510	4520	4530	4540	4550	4560	4570	4580	4590	4600	4610	4620	4630	4640	4650	4660	4670	4680	4690	4700	4710	4720	4730	4740	4750	4760	4770	4780	4790	4800	4810	4820	4830	4840	4850	4860	4870	4880	
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1060 ACACAGTGC

39. US-09-030-606-175 (1-1167)
US-08-904-809-20 Sequence 20, Application US/08904809

Initial Score	=	51	Optimized Score	=	213	Significance	=	0.26
Residue Identity	=	29%	Matches	=	231	Mismatches	=	.523
Gaps	=		Conservative Substitutions	=			=	0

CCAGAGTACAACAGAGCTTTTGCTCGCTAACGACCTCATGCTCATCAAGTTGGACGAATCGTGTCGAGTCT

40. US-09-030-606-175 (1-1167)
US-09-020-747-20 Sequence 20, Application US/09020747

Initial Score = 51 Optimized Score = 213 Significance = 0.26
Residue Identity = 29% Matches = 231 Mismatches = 523
Gaps = 19 Conservative Substitutions = 0

```
200 210 220 230 240 X 250 260
CCAGAGTACAACAGACTCTGTGCTCGTAAACGCTCATGCTCATCAAGTTGGACGAATCCGTTGCCGAGTCT
                TTTTTTTTTTTTTTTTTTTT
                X 10 20

270 280 290 300 310 320 330
GACACATCCGAGCATCAGATTCCTTCGAGTGCCCTACCGCGGGAATCTTTCCTCGTNTCTGGCTGG
|||||
AAACCCCTCCATTNAATGNAACATTCGGAATGTCCAAACCCCTCTNTCCAAATNCCNTTCCCGGNGG
30 40 50 60 70 80 90

340 350 360 370 380 390 400 410
GGTCTGCTGGCGAAGCGGAGAGTCTACCGTGTGCTGCACTGCTGCAAGCTGTCGGTGTCTGAGGANGTC
|||||
GGTTCCAAACCCCAANTTANNTTGGANNTTAAATTAATNTTNTTGGGNNNAACCCNAATGTNANGAA
100 110 120 130 140 150 160

420 430 440 450 460 470 480
TGCAGTAAGCTTATGACCGCTGTACACCCAGCATGTTCTGCGCGGGGAGGCAAGACAGAGGAC
|||||
AGTTNACCCCAANTATNANC-----TTNATNCCCTGGAACCGTNGTNTCCAAATNTTAAACCCCTTAANT
170 180 190 200 210 220 230

490 500 510 520 530 540 550
TCCCTCAACGGTGACTCTGGGGGCCCTGTATCGCAACGGTACTTCGAGGGCCTTGTCTTCGGAAGA
|||||
CCCTCGGAATNGTNGGAAACCCCAANTTCTGNTAAGTGTGTTGAAGNTNAAATNAAANCCNCCA
240 250 260 270 280 290 300

560 570 580 590 600 610 620
GCCCGGTGTGGCAACTTGGGCTGCGAGGTGTCTACACCAACCTCTGCAAAATCTACTGAGTGATAGAAA
|||||
ATTGTTTTTNGCCAGCGCTGAATTAATTGGNTCCGNTGTTTCCNTTAAANAAGNNANCCCGGTANT
310 320 330 340 350 360 370

630 640 650 660 670 680 690
ACCGTCCAGNCCAGTTAACTCTGGGACTGGGAACCCATGAAATTTGACCCCAATATCATCTCGCGGAAGA
|||||
NAATCCCCCNCCCAANTTATACCGANTTTTTTTTNGAATGGGANCNCNGGGGAATTAACGGGGNNNTCC
380 390 400 410 420 430 440

700 710 720 730 740 750 760 770
ATTTCAGGAATATCTGTTCCAGCCCTCTCTCCCTCAGGCGCCAGGAGTCCAGGCCCCCGCCCTCTCCCTC
|||||
CTNTTGGGGGCGNGNCCGCCCTCTCGGGGTNGGNCAGGNCNNAATGTTTAAGGTCGCAAAAATC
450 460 470 480 490 500 510 520

780 790 800 810 820 830 840
AAACCAAGGGTACAGATCCCAAGCCCTCTCCCTCCATCAGCCAGGAGTCCAGAGTCCAGCCCGCCCTCTCCN
|||||
CCTCCAGAAAAAANCTCCAG-----GNTGAGNTNGGTTTNGCCCTCTCCCTCCCGCCCGCCCTCTCG
530 540 550 560 570 580 590

850 860 870 880 890 900 910
TCAGACCCAGGAGTCCAGCCCTCTCTCCNTCAGACGCGAGGAGTCCAGACCCCGCCCGCCCTCTCCCTCAG
|||||
NANAGTTGGGTTTGGGGGCTGGGATTTTNTTCCCTCTNTTCCCTCTCCCTCCCGCCCGCCCTCTCG
590 600 610 620 630 640 650

920 930 940 950 960 970 980
CCGAGGGGTGAGGCGCCCAACCCCTCTCTCCNTCAGAGTCCAGAGTCCAGCCCGCCCAACCCCTCTCCCA
|||||
GGTTNGCTTTGTTGTCNNGGCCCGCCNCCNAGACTTTNCCGANTTAAATCCNTGCTCTGCGGAGT
660 670 680 690 700 710 720
```

```
990 1000 1010 1020 1030 1040 1050
GACCAGAGGTNCAGGTCCCGAGCCCTCTCTCCCTCAGACCCAGCGTCCAAATGCCACCTAGANTTCCCTGT
|||||
CCNTTGNAGGNTAAANGCCCGCTNNCGG
730 740 750 X
```

1060
ACACAGTGC

41. US-09-030-606-175 (1-1167)
US-09-020-747-26 Sequence 26, Application US/09020747

Initial Score = 51 Optimized Score = 250 Significance = 0.26
Residue Identity = 31% Matches = 261 Mismatches = 559
Gaps = 15 Conservative Substitutions = 0

```
180 190 200 210 220 X 230 240
GAGGCCAGCCTCTCGTACGGCACCCAGAGTACAACAGACTTCTGCTGCTAACGACCTCATGCTCATCAAG
                |||
                ANATTANTACAGTGAATCTTT
                X 10 20

250 260 270 280 290 300 310
TTGGACGAATCCGTTCTCGAGTCTGCACACCATCCCGAGCATCAGCATGCTTTCGAGTGCCCTACCGCGGG
|||||
TCCCAGAGGTGTGTANAGGAACGGGGCTAGAGCATCCCAAGATANTCTTATANCACACTGCTTTGACC
30 40 50 60 70 80 90

320 330 340 350 360 370 380
AACTTTCGCTGTTCTGCTGCTGGGCTGCTGCGGAGCGGAGCATGCTACCTGCTGCTGCTGCTGCTGCTG
|||||
AAGACTGCTGCGGACATTTCTCTGAGAAAGTGTGCGTCCCATCTCACTCTCTCTCTCTCTCTCTCTCTCC
100 110 120 130 140 150 160

390 400 410 420 430 440 450
GTGTCGGTGGTGTCTGAGGANGTCTGCAAGTCTATGACCCGCTGTACCCCGCTGTACCCCGCTGTGCGCC
|||||
AGAGGGGTGAGTAGCATCANGCCTTCGGTGGGAGGAGTCAAGGAAACAACANACCACAGAGCANACAGAC
170 180 190 200 210 220 230

460 470 480 490 500 510 520 530
GCGGAGGCAAGACCAAGGACTCTCTGCAACGGTGAATCTGCGGGGCGCTGTCTCAACAGGGTACTTG
|||||
CANTGATGACCATGGCGGAGCGAGCCTCTTCCCTGNAACGGGTGGGANGANGANGANGANGANGANGANG
240 250 260 270 280 290 300 310

CAGGCGCTGTGCTTTTCGGAAGCCCGCTGTGCGCAACTTGGCGTGGCAGGTGTCTACACCAACCTCTGC
|||||
CACACTATAACGTTTAAGCAGCCNAG---ATNANACCTGCTTCAAGTGCACCTCTCTCTACCTGACNACCAG
320 330 340 350 360 370

610 620 630 640 650 660 670
AAATTCAGTGTGATGAGAAACCGTCCAGNCCAGTTAACTCTGGGAGTGGGAAACCTATGAAATGAC
|||||
GACCNNAACCTGCNCGCTGGGACAGCNCCTGGGANCAGCTAAC-----NNAGCACTCACTGCC
380 390 400 410 420 430

680 690 700 710 720 730 740
CCCCAAATACATCTTCCGGAANGAATTCAGGAATATCTGTTCCAGCCCTCTCTCCCTCAGCCCGCTGAGT
|||||
CCCCATGGCCGTCNCGCTGGTGGTCTGNCAGGAAGTCCCTCTGTTGGAATTCGCGGAGNACCAAGGAGAN
440 450 460 470 480 490 500 510

750 760 770 780 790 800 810
CAGGCCCCAGCCCTCTCTCTCAACCAAGGTACAGATCCCGAGCCCTCTCTCTCTCTCTCTCTCTCTCTCT
|||||
CCCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT
520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000
```


42. US-09-030-606-175 (1-1167) Application US/09020747

100 110 120 130 140 150 160
 ACTGTTTCCAGAAATCCTTACACCATCGGGCTGGCGCTGCACAGCTTGTAGCGCCACCAAGAGCCAGGAGCC
 |||||
 CCTGTGCGGGCTCTGTAAGAGGAGTTCAGAGGTGAGAGCTCAAGAGCTTGCAGCATTGTTCGCAATCCTCT
 30 40 50 60 70 80 90
 170 180 190 200 210 220 230
 AGATGGTGGAGGCCACCGCTTCCGTACGGCACCCAGAGTAGTACACAGACTTGTCTCGCTAAACGACCTCATTC
 |||||
 CCANAGCANAGGAGAACCTACATCCCCCTAGAAGACACACCATTTGGAGTCTCTGGGAGGGGGAGTAGTGG
 100 110 120 130 140 150 160
 240 250 260 270 280 290 300
 TCATCAAGTTTGGACGAATCCGTCTCGAGTCTGACACCATCCGGAGCATCAGCATTGTTCGAGTGCCTCTA
 |||||
 GGTGGCATTTGATGTATCTTGTCCACCTGTAATGAAGAGCCAGAG----AGGAANGAGACGAANATGANAT
 170 180 190 200 210 220 230
 310 320 330 340 350 360 370
 CCGCGGGGAATCTTTGCTCTGNTTCTGGCTGGGGTCTGCTGGCGAAGCGGCAGAAATGCCCTACCGTCTGCTGCAT
 |||||
 TGGCCCTTCAAAGCTTAGGGGTCTGGCAGGTGGA
 240 250 260 270
 X

43. US-09-030-606-175 (1-1167) Application US/09020747

590	600	610	620	630	640
-----	-----	-----	-----	-----	-----

44. US-09-030-606-175 (1-1167)

Initial Score	=	50	Optimized Score	=	166	Significance	=	0.25
Residue Identity	=	29%	Matches	=	177	Mismatches	=	413
gaps	=	14	Conservative Substitutions	=			=	0

GACTCCTCGACAGGTGACTCTGGGGGGCCCTGATCGACACGGGTACTTCAGGGCCCTGTGTCTTTTCGGA
 490 500 510 520 530 540 550
 — — — — —
 ACTTTTATTAAATGTTTATA
 10 20

[illegible]

700 710 720 730 740 750 760
NGAATTTCAGGATATCTGTTCCAGCCCTCTCCCTCAGGCCAGGAGTGCAGGCCCCAGGCCCTCTCTCC
700 710 720 730 740 750 760
TCRAAGCAGGAAAA--TGANTATACCTAATTGCACAAATGGAATCAATTTTAATGTGAATTGCACATTATCC
770 780 790 800 810 820 830 840
CTCAAAACCAAGGTCAGATCCCGCCCTCTCCCTCAGACCCAGAGTCCAGACCCCCAGCCCTCCT
770 780 790 800 810 820 830 840
TTTAAAGCTTCTCAAANAANAATTTATTCAGCTCTAATTAATCAACACAGTGTAAATGGTTCAGGATAA
240 250 260 270 280 290 300

770 780 790 800 810 820 830 840
 CTCAAACACAGGGTACAGATCCCGCCCTCTCCCTCAGACCAGGAGTCCAGACCCCCAGCCCTCCT
 TTTTAAAGCTTTCAAANAANAANAATTATTCAGTCTANTTAATTCAAACAGCTGTTAAATGGTATCAGGATAA

TCAGGCTCGATGTCATAGTGTCTGGAAAGCGCGCTGTACCTTCGCTAG-----GGGCACACCCGTCAGGGCCGCTG
170 180 190 200 210 220 230

CGAGTCTCAGACACCATCCGGAGCATCAGCAATGCTTCGCACTGCCCTACCGGGGAACTCTTGCTCGTGTWTC
270 280 290 300 310 320 330
CAGAGCTGGGAGACATCCCGGAGTACGAACAGCGCTTAAAGTCTGGAGCGGGAGGTCCAGCAGTGTAGCGGC
170 180 190 200 210 220 230
0
340 350 360 370 380 390 400
TGCTGGGTGCTGTGGCGAAGCAAGTACGCTACGCTGCTGCACCTCGTGAAGTCTCGGTGGTGTGTCTGA
|||||
GTCTGGGTGGGTGGCGGA--NGCCTGANCCTCTGCTCTTGCTGCCGCCANGTGGGCCGCCACACCCCTCTGA
240 250 260 270 280 290 300
410 420 430 440 450 460 470
GGANGTCTGCAGTAAGTCTATGACCCCGCTGTACCAACCCCGAGCATCTTCTGCGCCGCGGAGGCAAGACCA
|||||
CCTGCTGTGGTCCAAACACTAGAGCCCTGCTGGGGACTTCAAGANANACCCCAACANGGGGATTTTGTCTCT
310 320 330 340 350 360 370
480 490 500 510 520 530 540
GAAGGACTCCTGCAACGGTGACTTGGGGGCCCTGATCTGCAACGGGTACTTGCAGGGCTTGTGTCTTT
|||||
ANANTAAGCTCATCTGGGGCTCGGGCCCCCGACCTCGGTGGGCTTGTCTTTGANGTGAAGCCCATGTCAT
380 390 400 410 420 430 440
550 560 570 580 590 600 610 620
CGAAAGCCCGTGTGGCCCACTTGGCGTCCAGGTGTCTACACCAACTCTGCAAAATCACTGAGTGGAT
|||||
CTG--GGCCACTGTGNGACCACTTTGGGAGTGTCTC---CTTACACCAACANNATGCGCGCTCTC
450 460 470 480 490 500 510
520 530 540 550 560 570
AGAAACCGTCCAGNCCAGTTAACTCTGGGACTGGGAACCCATGAAATTGACCCCAATACTCATCTCTG
|||||
CGGAACACANTCCCAACCTGNGAAGGATCAAGNCTGNATCC-----ACTNNTNCTANAACCGGC
520 530 540 550 560 570
700 710 720 730 740 750 760
GGRANGAATTCAGGAATATCTGTTCAGACCCCTCTCCCTCAGGCCCGCAGGTCCAGGCCGCCAGCCCTC
|||||
CNCNCGGNGTGGAACCCNCTTTGTCTTTCNTNAGGGTTAATNCGGCTTGGCCTTNCANNCTC
580 590 600 610 620 630 640
770 780 790 800 810 820 830
CTCCCTCAAACCAAGGTACAGATCCCGAGCCCTCTCTCTCAGCCAGGAGTCCAGACCCCGCCAGCCGCC
|||||
CTNCNCTTTTCCNNTGTTNAAATCTTTANGCNCNCCNCTCCCNMNCNANANCCGACCCNNANNTTN
650 660 670 680 690 700 710
840 850 860 870 880 890 900
TCNTCNTCAGACCCAGGAGTCCAGGCCCTCTCTCNTCAGAGCAGGAGTCCACACCCCGCCAGCCNCTCNTC
|||||
NANNNCTGGGGGTNCCNNGANGATTGACCCNCCNCCCTNTANTTGCNTTNGGNNCNGTGGCCCTTCTCCT
720 730 740 750 760 770 780
910 920 930 940 950 960
CGTCAAGCCAGGGGTCCAGGCCCAACCCCTCNTCTCAGAGTCAGAGTCCAGAGTCCAAAGCCC
|||||
CTNNGGANNCG
980 990 X

48. US-09-030-606-175 (1-1167) 36 Application US/088006596

=	50	Optimized Score	=	256	Significance	=	0.25
=	35%	Matches	=	302	Mismatches	=	508
=	36	Conservative Substitutions	=			=	0
		Gaps					

GGCCTGCACAGCTTTGAGGCCGACCAAGAGGCCAGGGCCAGATGTTGAGGCCAGCCTCTCCGTACGGCAC

[illegible]

47. US-09-030-606-175 (1-1167)
US-09-030-747-8 Sequence 8.
Application US/09020747

-	Initial Score	=	50	Optimized Score	=	256	Significance	=	0.25
-	Residue Identity	=	34%	Matches	=	286	Mismatches	=	513
-	Gaps	=	26	Conservative Substitutions	=			=	0

CTGCTCGGGCGCTCTGTGTGATCCGAGTGGTGCTGCACCGCGACACTGTTTCGAGNACTCCTACACAT
 CATTTCGGGGTTACTTCTTAA
 X
 10 20

CGGGTGGGCTGCACAGCTTTGAGCGCCACCAGACCGGAGCCAGATGTGGAGCCAGCTCTCCGT
GGAAGCCGAGCGGAGCTGCTAACCTGGGAATCGGTGCATAAGGAGAACTTTCTCTGGCAGCGCTAGGG

[illegible]

[illegible][illegible]

> O <
O | O Intelligence
> O <

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file us-09-030-606-175-inv.res made by tport on Thu 1 May 103 15:05:56-PDT.

Query sequence being compared: US-09-030-606-175' (1-1167)
Number of sequences searched: 410
Number of scores above cutoff: 410

Results of the initial comparison of US-09-030-606-175' (1-1167) with:

File : 6130043.seq
File : 6252047.seq
File : US0806596.seq
File : US08850713.seq
File : US08904809.seq
File : US09020747.seq
File : US09841894A.seq

100-

N -

U 50-

M -

B -

E -

R -

O -

F 10-

S -

E 5-

Q -

U -

N -

E -

C -

E -

S 0-

SCORE 0

STDEV -1

11

22

32

43

54

65

75

86

97

PARAMETERS

Similarity matrix Unitary K-tuple
Mismatch penalty 1 Joining penalty 4
Gap penalty 5.00 Window size 30
Gap size penalty 0.33
Cutoff score 0
Randomization group 0

SEARCH STATISTICS

Scores: Mean 30 Median 30 Standard Deviation 15.37
Times: CPU 00:00:00.99 Total Elapsed 00:00:01.00

Number of residues: 189792
Number of sequences searched: 410
Number of scores above cutoff: 410

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Init. Opt.
1. US-09-020-747-17	Sequence 173, Application 1265	97	386	4.36
2. US-08-904-809-9	Sequence 9, Application 801	91	239	3.97
3. US-09-020-747-11	Sequence 110, Application 3410	90	399	3.90
4. US-09-020-747-12	Sequence 120, Application 90	87	89	3.71
5. US-09-020-747-17	Sequence 175, Application 1167	82	384	3.38
6. US-09-020-747-17	Sequence 174, Application 1459	69	373	2.54
7. US-09-020-747-9	Sequence 9, Application 801	63	239	2.15
8. US-09-020-747-16	Sequence 168, Application 273	62	95	2.08
9. US-09-020-747-13	Sequence 133, Application 278	62	90	2.08
10. US-09-020-747-17	Sequence 171, Application 1248	62	382	2.08
11. US-09-071-710-8	Sequence 8, Application 342	61	117	2.02
12. US-09-525-397-8	Sequence 8, Application 342	61	117	2.02
13. US-09-841-894A-8	Sequence 8, Application 342	61	117	2.02
14. US-09-071-710-16	Sequence 16, Application 2152	61	390	2.02
15. US-09-525-397-16	Sequence 16, Application 2152	61	390	2.02
16. US-09-841-894A-1	Sequence 16, Application 2152	61	390	2.02
17. US-08-904-809-65	Sequence 65, Application 377	60	121	1.95
18. US-09-020-747-65	Sequence 65, Application 377	60	121	1.95
19. US-08-904-809-47	Sequence 47, Application 774	60	260	1.95
20. US-08-806-596-9	Sequence 9, Application 801	58	239	1.82
21. US-09-071-710-15	Sequence 15, Application 2143	57	391	1.76
22. US-09-525-397-15	Sequence 15, Application 2143	57	391	1.76
23. US-09-841-894A-1	Sequence 15, Application 2143	57	391	1.76
24. US-09-071-710-6	Sequence 6, Application 195	56	71	1.69
25. US-09-525-397-6	Sequence 6, Application 195	56	71	1.69

1. US-09-030-606-175' (1-1167)

US-09-020-747-17 Sequence 173, Application US/09020747

Initial Score = 97 Optimized Score = 386 Significance = 4.36
Residue Identity = 37% Matches = 444 Mismatches = 711
Gaps = 40 Conservative Substitutions = 0

GCAGCCGCACTCGCAGCCCTGGCAGCGGCACCTGGTCATGGAACCAAGTAATTTCTGCTGGGGCTCTGTG
10 20 30 40 50 X 60 70
30 40 50 60 70 80 90
TTTATTTCTGGATCTAGGGGAAGGACAAAATGAAACCACTGGTAAGTTGGTCAACNTGCCACA
100 110 120 130 140 150 160
AGGGGCACTGTGTACAGGGANANTCTAGTGGCATTTGGACCGCTGGTCTCAGGACGAGGGCTGGAC-
170 180 190 200 210 220 230
-CTGNACCTCTGGTCTGGGGAACGAGGGTTGGGGCTTGGACCTCTCAGTCT-GANGANGAGGGTTGG
240 250 260 270 280 290
ACAGACCCCTGCTCGCTAACGACCTCATCTCAAGTTCAGCAATCCGTCGCCAGTCCACCATCC
220 230 240 250 260 270 280
GGGCTGCACCCCTGGTCTGACGGANGANGGGCTGGGGGTCTGGACTCT- - - - - GCGTCTGANGG


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670      680      690      700      710      720      730
CCC---CCAGAGTCACGTTGCAGAGTCTCTTCTGGCTTTCGCCCTCGCGCGCAGAACATGCTGGGGTGG
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
CCCTCTCTCTCTCCCGCAGTCTCTAGGGCTCCCTGACTGGAGGCTTCCAGAGGGGTTTTCAGTCTGCAGCTTA
950      960      970      980      990      1000      1010      1020

740      750      760      770      780      790
TACAGCGGGTC--ATAGAGCTTACTGCA--GACNTCTCAGACACACCACCGACAGCTTACGCACTGCAGCAC
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
TACAGGAGCGCCAGAGGGCTCCCATGACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGCTCAGGCT
1030     1040     1050     1060     1070     1080     1090

800      810      820      830      840      850      860
GGTAGGCAATTCGTGCGGTCGCGCAGCAGACCCAGCCCA-----GANACGAGGCAAGAGTTCCCGCGCG
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
TAACAGCTAGCCCTCTAGTTGAGACACACCTTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCACTCTGG
1100     1110     1120     1130     1140     1150     1160

870      880      890      900      910      920
TAGGGCACTGCGAAGC----AATGCTGATGCTCCGGATGGTGTGAGACTCGGACACGGAATTCGTCCAACTTG
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
TTTCCCATCTTAAGCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAA
1170     1180     1190     1200     1210     1220     1230

930      940      950      960      970      980      990      1000
ATGAGCATGAGGTCGTTAGGAGCAAGAGTCTGTTGACTCTGGGTGCGCTACGAGAGGCTGGCTCCACCC
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
ACACTCTCCATGGGATTTGAACATATGAAGTTATTGTAGGGAAGAGTCTTGAGGGGCAACACACAAGA
1240     1250     1260     1270     1280     1290     1300

1010     1020     1030     1040     1050     1060     1070
ATCTGGCTCCCTGGCTCTGGTGGCCCTCAAGACTGTGCGAGGCCAGCCCGATGGTGTAGGAGTTCTGGAAA
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
ACCAGGTCCTCTCAGCC--CACAGCACTGCTTTTGGCTGATCCACCCCTCTTACCTTTTATCAGGATG
1310     1320     1330     1340     1350     1360     1370

1080     1090     1100     1110     1120     1130     1140
CAG--TGTTGGGCTGACAGCACCACCTGCGGATGACAGCAGCAGCCGCGAGCAGAACATTCGTTTTCATGA
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
TGGCTCTGTGCTCTCTGTTGCCATCACAGACACAGGCAATTAATAATTTAACITATTATTATTAAACAA
1380     1390     1400     1410     1420     1430     1440     1450

1150     1160
CCAGTGGCGCTGCGAGGGCTGCGC
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
GTAGAAGGGAATCCATTGCTAGCTTTCTGTGTTGGTCTTAATATTGGTAGGGTGGGGATCCCAACA
1460     1470     1480     1490     1500     1510     1520

ATC

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15. US-09-030-606-175' (1-1167)

US-09-525-397-16 Sequence 16, Application US/09525397

Initial Score = 61 Optimized Score = 390 Significance = 2.02
 Residue Identity = 37% Matches = 452 Mismatches = 707
 Gaps = 40 Conservative Substitutions = 0

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CGTGTGACAGCTTTCACGCGCCCTCACGGGTTTCACTTCTCAGCCTTCTCAGCCTGTCAGATCCTGCCCTACACACTGCG
240     250     260     270     280     290     300

30      40      50      60      70      80      90
TTTATTTCTGGATCAGGGGAAAGGCAAAAAATGAAAAACCAACTGGTAGGTGGGTCAACNTGCCACA
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
CTCCCTCTACACCGGGGAGACAGAGTGTTCCTGCCAAAATACCGAGGGGACACTGGAGGTGCTAGCAGTGA
310     320     330     340     350     360     370

100     110     120     130     140     150     160
ATGAGCATGAGGTCGTTAGCGAGCAAGAGTCTGTTGTTACTCTGGGTGCGGTACGGAGAGGCTTGGCCTCCACC

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AGGGGCACTCTGTACAGGGANANTCTAGG-----TGGCAATTGGACCCGCTGGGTCTGAGGGAGAGGGCGCTG-
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
GGACAGCCTGATGATGACCACTTCTTCCAGGCGCTTAAAGCCTGGAGTCTCCCTTAATGAGACAGTGGGTGC
380     390     400     410     420     430     440     450

170      180      190      200      210      220
----GGACCTGNACCTCTGGGTCTGGGGAACAGGGGTTGGGGGTTGGACTCTGTGACTCTGANGGANGAGG
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
TGGAGGAGTGGCCTGTGTCTCCACCTCCACCGCGCTCTCGGGGCGCTCTGCTGTGTATGTTCTCCGTAGCTGT
460     470     480     490     500     510     520

230      240      250      260      270      280      290      300
GGTTGGGGGCTCGCACCCCTGGGTCTGACGGANGANGGCTGGGGGCTTGGACTCTTCCGTCTGANGGAGG
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
GGTGGTGGTGGCCTGTGTCTCCACCGCGCTCTCGGGGCGGGGCTGTGTCTGCTGCTGCTGCTGCTGCTGCTGGA
530     540     550     560     570     580     590     600

310      320      330      340      350      360      370
AGGGGCTGAGACTCTGGGTCTGANGANGAGGGGCTGGGGGCTTGGGCTCTTGGGTCTTGGAGGAGGAGGGG
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
TAGTGCCTTCTGCTGTCTCCAGGTGGGCCCATCCCT---GTTTATGGGCTCCATGTC-CAGCTCAGGACAGT
600     610     620     630     640     650     660

380      390      400      410      420      430      440
CTGGGATCTCTACCCCTGGTTTGGGGAGGAGGGGCTGGGGGCTTGGACTCTCTGGGCTTGGAGGAGGAGGG
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
CTGTCACTGCTCTATATGTTGTCTGCGCGAGGCTTGGGTCTGGTGGCTTGTGCTTGTATACACAG-GTAGTA
670     680     690     700     710     720     730

450      460      470      480      490      500      510
GCTGGGAACAGATATTCCTGAATTCNTTCCGAGGATGATATTGGGGTCAATTTTCATGGGTTCACATGCC
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
TTTACAGAGAGGAGCTTGGCCAAATACTCAGGTAGAAAATTCAGGACACATTTGGGGTGGAGGCTCGCTC
740     750     760     770     780     790     800

520      530      540      550      560      570      580
CAGAGTTAACTGGNCTGACGGTTTTCTCTATCCACTCAGTGAATTTCCAGAGGTTGGTGTAGACACCTGGC-
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
ACTGGGTCCAGCTCCCGCTCTCTGTTAGCCCATGGGGCTGCCCGGCTGGCGGCTTCTGTGTGTGCTGC
810     820     830     840     850     860     870

590      600      610      620      630      640      650      660
ACGCCAAGTTGGCACAGGGGCTTTCCGAAAGACACAAGCCCTGCAAGTACCCTGTGCAGATCAGAGGGC
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
AAAGTAAATGGGCTCTCTGCTGCCACCCCTGCTGCTGAGGTGCTGCTGACAGCTGGGGCTGGGGCGCT
880     890     900     910     920     930     940

CCC---CCAGAGTCACGCTTGCAGAGTCTCTTCTGGTCTTGCCTCCCGCGCGCAGAACATGCTGGGGTGG
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
CCCTCTCTCTCTCCCACTCTAGGGCTGCTGAGGCTGCTGAGGCGCTTCCAGGGGTTTCAAGTCTGGACTTA
950     960     970     980     990     1000     1010     1020

740      750      760      770      780      790
TACAGCGGGTC--ATAGAGCTTACTGCA--GACNTCTCAGACACACCACCGACAGCTTACCGAGTGCAGCAC
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
TACAGGAGCGCCAGAGGGCTCCCATGACTGGAATGCGGGGACTCTGCAGGTGGATTACCCAGGCTCAGGCT
1030     1040     1050     1060     1070     1080     1090     1100

800      810      820      830      840      850      860
GGTAGGCAATTCGTGCGGTCGCGCAGCAGACCCAGCCCA-----GANACGAGGCAAGAGTTCCCGCGCG
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
TAACAGCTAGCCTCTCTAGTTGAGACACACCTTAGAGAGGGTTTTTGGGAGCTGAATAAACTCAGTCACTG
1100     1110     1120     1130     1140     1150     1160

870      880      890      900      910      920
TAGGGCACTGCGAAGC----AATGCTGATGCTCCGGATGGTGTGAGACTCGGACACGGAATTCGTCCAACTTG
|||||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
TTTCCCATCTTAAGCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCATGGGAGTTTCTAGGATGAA
1170     1180     1190     1200     1210     1220     1230

930      940      950      960      970      980      990      1000
ATGAGCATGAGGTCGTTAGCGAGCAAGAGTCTGTTGTTACTCTGGGTGCGGTACGAGAGGCTGGCTCCACCC

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	890	900	910	920	930	940	950	
880	GCTGATGCTCGGATGGTGCAGACTCGGACACGGATTTCGTCCAACTTGATGAGCATGAGTGCGTTAGCGAG							
870	TCTGACTTGCCTGATTACTCAGCAATCTTGGAACAATCCCTGATTCGCCACTCCTTAGAG---GCRAGATAG							
860	560	570	580	590	600	610	620	
	960	970	980	990	1000	1010	1020	
850	CAAGAGTCTGTTGTACTCTGGTGGCGTACGAGAGGCTG--GGCTCACCATCTGGCTCCCTGGCTCTTGG							
840	GCTGTTAAGAGTAGGGCTGGACCACTTGGAGCCAGGCTGCTGGCTTCAAATTTNGCTCATTTACGAGCTA							
830	630	640	650	660	670	680	690	
	1030	1040	1050	1060	1070	1080	1090	
820	TCGGGCTCAAGACTGTGAGGCCACGCCGATGTTAGAGAGTCTCTGAAACAGTGTGCGGCTCAGACACC							
810	TGGGACCTTGGCAAGTNATCTTCACTTCTATGGGCNTCATTTGTTCTACCTGCAAAATGGGGGATAATAA							
	700	710	720	730	740	750	760	770
	1100	1110	1120	1130	1140			
	CATCTGGGATGCACCAGGACGCCCGCAGCAGAACAATTCGTTTTGCATGCCACGT							
	TAGT							
	X							

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20. US-09-030-606-175' (1-1167)
US-08-806-596-9 Sequence 9, Application US/08806596

Initial Score = 58 Optimized Score = 239 Significance = 1.82
Residue Identity = 33% Matches = 266 Mismatches = 514
Gaps = 24 Conservative Substitutions

300 310 320 330 340 350 360 370
AGGAGGGGCTGGACTCTCTGGGTGTGANGAGGGGCTGGGGGGTCTGGACTCTCTGGGTCTGAGGGAGGAG
      ||| ||| ||| ||| ||| ||| |||
ACGCTTTGATCTCTCCAGGCTG
      X      10      20

380 390 400 410 420 430
GGGCTGGGGATCTGTACCTTGGTTTGGAGGAGGGGCTGGGG---CTGACTCTCTGGGCTTGAGGGA
      ||| ||| ||| ||| ||| ||| |||
GGACTGGTTCTTGGGAGGACCGGCACTGTGTGTTTGAANGATGACACTCCCAAGAGTGGTCTCTGACAGT
      30      40      50      60      70      80      90

440 450 460 470 480 490 500 510
GGAGGGGCTGGGACAGATATCTCTGAATTCNTCCGAGGATGATTTTGGGGTCAATTTGATGGTGTCCC
      ||| ||| ||| ||| ||| ||| |||
GGCCAGATGGACATPGGGGCTCACTCAAGGACAAGGCCACCAGGTGGGGGGCGGAGCCACATGATGCTCT
      100      110      120      130      140      150      160

520 530 540 550 560 570 580
AGTCCCAGAGTAACTGNGCTGGACGGTTTTCTCTATCCACTCAGTGAATTTGCAGAGGTTGGTGTAGACA
      ||| ||| ||| ||| ||| ||| |||
TACTCTATGAGCAAAATCCCTCTGTGGGGGCTTCTCTCTTGAAGTCCGCCCANAGGCGCTCAGTCTTTGGACCCA
      170      180      190      200      210      220      230

590 600 610 620 630 640 650
CTGTGCACGCCCAAGTTGGCCACACGGGGCTTTTCCGAAAGACACAAGGCCCTG---CAAAGTACCCGTGACG
      ||| ||| ||| ||| ||| ||| |||
NGCAGTCTATGGGGTTGTGNNCCAACTGGGGGCCNCAACGCAAAANGGNCAGGSCCTTCGNCACACCATCCC
      240      250      260      270      280      290      300      310

660 670 680 690 700 710 720
ATCAGGGGCCCCCAGAGTCAACCGTTTGCAGGAGTCTCTTCTGGTCTTGCCCTCCGCGGCGCAGAACATGCTG
      ||| ||| ||| ||| ||| ||| |||

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ANGACGGCGGTACACTNCTGTGAGCCTCC	320	330	340	350	360	370	380
730	740	750	760	770	780	790	
GGTGGTACAGCGGGTCATAGAGCTTACT	390	400	410	420	430	440	450
ANCTGTTTCNGTCCNACCTCCANCCTTCT	800	810	820	830	840	850	860
ACGGTAGGCATTTCTGCC-----GTT	ACGGTAGGCATTTCTGCC	870	880	890	900	910	920
CGGACCTT-----CGGACGAACTGCT	CGGACCTT-----CGGACGAACTGCT	930	940	950	960	970	980
TTGATGAGCATGAGGTGGTTAGCGAGCA	TTGATGAGCATGAGGTGGTTAGCGAGCA	990	1000	1010	1020	1030	1040
ACCATCTGGCTCCCTGGCTCTTGGTGG	ACCATCTGGCTCCCTGGCTCTTGGTGG	1050	1060	1070	1080	1090	1100
AAACAGTGTGGCGGTGACAGCACCCACT	AAACAGTGTGGCGGTGACAGCACCCACT	1110	1120	1130	1140	1150	1160
ACCGAGTGTGGCGGTGACAGCACCCACT	ACCGAGTGTGGCGGTGACAGCACCCACT	1170	1180	1190	1200	1210	1220
NCNRAAAGGGCCNNNANCAATCTCTTNC	NCNRAAAGGGCCNNNANCAATCTCTTNC	1230	1240	1250	1260	1270	1280
CCCTCGMCCNTNCCCCNTTAATCCNCCT	CCCTCGMCCNTNCCCCNTTAATCCNCCT	1290	1300	1310	1320	1330	1340
TTGANCCTCCNTTTTAAANNACNTT---	TTGANCCTCCNTTTTAAANNACNTT---	1350	1360	1370	1380	1390	1400
CTTCCCTNTTAAAGGGTTGANCCTCCG	CTTCCCTNTTAAAGGGTTGANCCTCCG	1410	1420	1430	1440	1450	1460
GGGCACCTT-----CGGACGAACTGCT	GGGCACCTT-----CGGACGAACTGCT	1470	1480	1490	1500	1510	1520
CGGACCTT-----CGGACGAACTGCT	CGGACCTT-----CGGACGAACTGCT	1530	1540	1550	1560	1570	1580
TTGATGAGCATGAGGTGGTTAGCGAGCA	TTGATGAGCATGAGGTGGTTAGCGAGCA	1590	1600	1610	1620	1630	1640
ACCATCTGGCTCCCTGGCTCTTGGTGG	ACCATCTGGCTCCCTGGCTCTTGGTGG	1650	1660	1670	1680	1690	1700
AAACAGTGTGGCGGTGACAGCACCCACT	AAACAGTGTGGCGGTGACAGCACCCACT	1710	1720	1730	1740	1750	1760
NCNRAAAGGGCCNNNANCAATCTCTTNC	NCNRAAAGGGCCNNNANCAATCTCTTNC	1770	1780	1790	1800	1810	1820
CCCTCGMCCNTNCCCCNTTAATCCNCCT	CCCTCGMCCNTNCCCCNTTAATCCNCCT	1830	1840	1850	1860	1870	1880
TTGANCCTCCNTTTTAAANNACNTT---	TTGANCCTCCNTTTTAAANNACNTT---	1890	1900	1910	1920	1930	1940
CTTCCCTNTTAAAGGGTTGANCCTCCG	CTTCCCTNTTAAAGGGTTGANCCTCCG	1950	1960	1970	1980	1990	2000
GGGCACCTT-----CGGACGAACTGCT	GGGCACCTT-----CGGACGAACTGCT	2010	2020	2030	2040	2050	2060
CGGACCTT-----CGGACGAACTGCT	CGGACCTT-----CGGACGAACTGCT	2070	2080	2090	2100	2110	2120
TTGATGAGCATGAGGTGGTTAGCGAGCA	TTGATGAGCATGAGGTGGTTAGCGAGCA	2130	2140	2150	2160	2170	2180
ACCATCTGGCTCCCTGGCTCTTGGTGG	ACCATCTGGCTCCCTGGCTCTTGGTGG	2190	2200	2210	2220	2230	2240
AAACAGTGTGGCGGTGACAGCACCCACT	AAACAGTGTGGCGGTGACAGCACCCACT	2250	2260	2270	2280	2290	2300
NCNRAAAGGGCCNNNANCAATCTCTTNC	NCNRAAAGGGCCNNNANCAATCTCTTNC	2310	2320	2330	2340	2350	2360
CCCTCGMCCNTNCCCCNTTAATCCNCCT	CCCTCGMCCNTNCCCCNTTAATCCNCCT	2370	2380	2390	2400	2410	2420
TTGANCCTCCNTTTTAAANNACNTT---	TTGANCCTCCNTTTTAAANNACNTT---	2430	2440	2450	2460	2470	2480
CTTCCCTNTTAAAGGGTTGANCCTCCG	CTTCCCTNTTAAAGGGTTGANCCTCCG	2490	2500	2510	2520	2530	2540
GGGCACCTT-----CGGACGAACTGCT	GGGCACCTT-----CGGACGAACTGCT	2550	2560	2570	2580	2590	2600
CGGACCTT-----CGGACGAACTGCT	CGGACCTT-----CGGACGAACTGCT	2610	2620	2630	2640	2650	2660
TTGATGAGCATGAGGTGGTTAGCGAGCA	TTGATGAGCATGAGGTGGTTAGCGAGCA	2670	2680	2690	2700	2710	2720
ACCATCTGGCTCCCTGGCTCTTGGTGG	ACCATCTGGCTCCCTGGCTCTTGGTGG	2730	2740	2750	2760	2770	2780
AAACAGTGTGGCGGTGACAGCACCCACT	AAACAGTGTGGCGGTGACAGCACCCACT	2790	2800	2810	2820	2830	2840
NCNRAAAGGGCCNNNANCAATCTCTTNC	NCNRAAAGGGCCNNNANCAATCTCTTNC	2850	2860	2870	2880	2890	2900
CCCTCGMCCNTNCCCCNTTAATCCNCCT	CCCTCGMCCNTNCCCCNTTAATCCNCCT	2910	2920	2930	2940	2950	2960
TTGANCCTCCNTTTTAAANNACNTT---	TTGANCCTCCNTTTTAAANNACNTT---	2970	2980	2990	3000	3010	3020
CTTCCCTNTTAAAGGGTTGANCCTCCG	CTTCCCTNTTAAAGGGTTGANCCTCCG	3030	3040	3050	3060	3070	3080
GGGCACCTT-----CGGACGAACTGCT	GGGCACCTT-----CGGACGAACTGCT	3090	3100				

...21. US-09-030-606-175' (1-1167)

US-09-030-606-175, (I-1167)
US-09-071-710-15 Sequence 15 Application US/09071710

Initial Score	=	57	Optimized Score	=	391	Significance	=	1.76
Residue Identity	=	37%	Matches	=	448	Mismatches	=	711
Gaps	=		Conservative Substitutions	=	39		=	0

30 40 50 60 70 80 90
 TTTATTTCTGGATCTAGGGAAAGGGACAAAAATGAAACCAACTGTTAAGGTTGGGTCAACNTGCCACA
 230 240 250 260 270 280 290 300
 CGTGGTGACAGCTTCAGCCGCCCTCACCGGGTTCACTTCTCAGCCCTGCAGATCTTGCCTCCTACACACTGGC
 310 320 330 340 350 360 370
 TTTTCTTTTGGCGCTTCTCTTANAC
 X + 10 20

[illegible]

[illegible]

Initial Score	=	56	Optimized Score	=	71	Significance	=	1.69
Residue Identity	=	38%	Matches	=	75	Mismatches	=	118
Gaps	=	2	Conservative Substitutions	=				0

80	90	100	110	120	130	140	150	
GGGTCAACNTGCCACAAGGGGCAC	TGTTACAGGANANTCTAGTGGCAT	TGGACCCCTGGGTCTGAGG						
					CTTGGCCAAATACTCAGCGTAG			
					X	10	20	

150	170	180	190	200	210	220	
AGGAGGGCTGGGACCTGNACCTCTGGGTCTGGGGAACGAGGGTTGGGGCTTGGACCTCT--GACTCTGA							
AAACCTCCAGCACATTTGGGGTGGAGGGCGCTGCTCACCTGGGTCCAGCTCCCGCTCTGTTAGCGCCATG							
30	40	50	60	70	80	90	

230	240	250	260	270	280	290	
NGGAGGAGGGTTGGGGCTCGACCCCTGGGTCTGACGGANGGGCTGGGGGTCTGGACTCTTGCGCT							
GGCTCGCGGCTGGCGCCAGTTCTGTTGCTGCCAAAGTAATGTGGCTCTCTGCTGCCACCCCTGTGCTGC							
100	110	120	130	140	150	160	

300	310	320	330	340	350	360	
TGANGAGGAGGGCTGGACTCTCTGGGTCTGANGGANGAGGGCTGGGGGGTCTGGACTCTTGGGTCTGAGG							
TGAGGTCCGTANTGCACAGCTGGGGCTG							
170	180	190	X				

370	
GAGCAGG	

[illegible]

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24. US-09-030-606-175' (1-1167)
US-09-071-710-6 Sequence 6, Application US/09071710

Initial Score = 56 Optimized Score = 71 Significance = 1.69
Residue Identity = 38% Matches = 118 Mismatches = 118
Gaps = 2 Conservative Substitutions = 0

      80      90      100      110      120      130      140      150
GGGTCAACWTGCCACAGGGGCGCACTGTTCTACAGGANANTCTAGTGCATATGGACCCCTGGGCTCTGAGG
|||||
CTTGCCCAATAACTACGCGTAG
X
      10      20

      160      170      180      190      200      210      220
AGGAGGGCTGGGACCTGNACCTCTGGGCTGGGAACGAGGGTTGGGGCTTGACACTCT--GACTCTGA
|||||
AAACTTCAGCACATATGGGGTGGAGGGCTGCTCCTACATGGTCCCGCTCTCTGTTAGCCCGCATG
30 40 50 60 70 80 90

      230      240      250      260      270      280      290
NGNAGAGGGGTTGGGGGCTGCACCCCTGGGTCTCAGCGANGAGGGCTGGGGGTCTGGACTCTCGTGGCT
|||||
GGGTGCCGGGCTGCCCGCAGTTTCTGTGTCTGCCAAAGTAATGTGGGCTCTCTGTGCCACCCCTGTGCTG
100 110 120 130 140 150 160 170

      300      310      320      330      340      350      360
TGANGAGGAGGGGCTGGACTCTCTGGGCTGANGGANGAGGGGCTGGGGGTCTTGGACTCTGGGCTCTGAGG
|||||
TGAGTGGCGTANTGACACACTGGGGCTG
170 180 190 X

370
GAGGAG

```

25. US-09-030-606-175' (1-1167)
US-09-525-397-6 Sequence 6, Application US/09525397

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Scores:	Mean	Median	Standard Deviation
	31	28	56.61

290 300 310 320 330 340 350 360
ATCAGATTGCTTCGAGTGCCTTACCGGGGAATCTTGCCTCGTTCTGGCTGGGGTCTGCTGGCGAAC

Gaps - 81 Conservative Substitutions = 0

GGCAGCAAAATCATATAACGGGAGGAGCTGCAGCCCGCAGCTCGCAGCCCTGGCAGGGGCACTGGTCAATGAA
10 20 30 40 50 60 70 80 90 100 110 120 130 140 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330 1340 1350 1360 1370 1380 1390 1400 1410 1420 1430 1440 1450 1460 1470 1480 1490 1500 1510 1520 1530 1540 1550 1560 1570 1580 1590 1600 1610 1620 1630 1640 1650 1660 1670 1680 1690 1700 1710 1720 1730 1740 1750 1760 1770 1780 1790 1800 1810 1820 1830 1840 1850 1860 1870 1880 1890 1900 1910 1920 1930 1940 1950 1960 1970 1980 1990 2000 2010 2020 2030 2040 2050 2060 2070 2080 2090 2100 2110 2120 2130 2140 2150 2160 2170 2180 2190 2200 2210 2220 2230 2240 2250 2260 2270 2280 2290 2300 2310 2320 2330 2340 2350 2360 2370 2380 2390 2400 2410 2420 2430 2440 2450 2460 2470 2480 2490 2500 2510 2520 2530 2540 2550 2560 2570 2580 2590 2600 2610 2620 2630 2640 2650 2660 2670 2680 2690 2700 2710 2720 2730 2740 2750 2760 2770 2780 2790 2800 2810 2820 2830 2840 2850 2860 2870 2880 2890 2900 2910 2920 2930 2940 2950 2960 2970 2980 2990 3000 3010 3020 3030 3040 3050 3060 3070 3080 3090 3100 3110 3120 3130 3140 3150 3160 3170 3180 3190 3200 3210 3220 3230 3240 3250 3260 3270 3280 3290 3300 3310 3320 3330 3340 3350 3360 3370 3380 3390 3400 3410 3420 3430 3440 3450 3460 3470 3480 3490 3500 3510 3520 3530 3540 3550 3560 3570 3580 3590 3600 3610 3620 3630 3640 3650 3660 3670 3680 3690 3700 3710 3720 3730 3740 3750 3760 3770 3780 3790 3800 3810 3820 3830 3840 3850 3860 3870 3880 3890 3900 3910 3920 3930 3940 3950 3960 3970 3980 3990 4000 4010 4020 4030 4040 4050 4060 4070 4080 4090 4100 4110 4120 4130 4140 4150 4160 4170 4180 4190 4200 4210 4220 4230 4240 4250 4260 4270 4280 4290 4300 4310 4320 4330 4340 4350 4360 4370 4380 4390 4400 4410 4420 4430 4440 4450 4460 4470 4480 4490 4500 4510 4520 4530 4540 4550 4560 4570 4580 4590 4600 4610 4620 4630 4640 4650 4660 4670 4680 4690 4700 4710 4720 4730 4740 4750 4760 4770 4780 4790 4800 4810 4820 4830 4840 4850 4860 4870 4880 4890 4900 4910 4920 4930 4940 4950 4960 4970 4980 4990 5000 5010 5020 5030 5040 5050 5060 5070 5080 5090 5100 5110 5120 5130 5140 5150 5160 5170 5180 5190 5200 5210 5220 5230 5240 5250 5260 5270 5280 5290 5300 5310 5320 5330 5340 5350 5360 5370 5380 5390 5400 5410 5420 5430 5440 5450 5460 5470 5480 5490 5500 5510 5520 5530 5540 5550 5560 5570 5580 5590 5600 5610 5620 5630 5640 5650 5660 5670 5680 5690 5700 5710 5720 5730 5740 5750 5760 5770 5780 5790 5800 5810 5820 5830 5840 5850 5860 5870 5880 5890 5900 5910 5920 5930 5940 5950 5960 5970 5980 5990 6000 6010 6020 6030 6040 6050 6060 6070 6080 6090 6100 6110 6120 6130 6140 6150 6160 6170 6180 6190 6200 6210 6220 6230 6240 6250 6260 6270 6280 6290 6300 6310 6320 6330 6340 6350 6360 6370 6380 6390 6400 6410 6420 6430 6440 6450 6460 6470 6480 6490 6500 6510 6520 6530 6540 6550 6560 6570 6580 6590 6600 6610 6620 6630 6640 6650 6660 6670 6680 6690 6700 6710 6720 6730 6740 6750 6760 6770 6780 6790 6800 6810 6820 6830 6840 6850 6860 6870 6880 6890 6900 6910 6920 6930 6940 6950 6960 6970 6980 6990 7000 7010 7020 7030 7040 7050 7060 7070 7080 7090 7100 7110 7120 7130 7140 7150 7160 7170 7180 7190 7200 7210 7220 7230 7240 7250 7260 7270 7280 7290 7300 7310 7320 7330 7340 7350 7360 7370 7380 7390 7400 7410 7420 7430 7440 7450 7460 7470 7480 7490 7500 7510 7520 7530 7540 7550 7560 7570 7580 7590 7600 7610 7620 7630 7640 7650 7660 7670 7680 7690 7700 7710 7720 7730 7740 7750 7760 7770 7780 7790 7800 7810 7820 7830 7840 7850 7860 7870 7880 7890 7900 7910 7920 7930 7940 7950 7960 7970 7980 7990 8000 8010 8020 8030 8040 8050 8060 8070 8080 8090 8100 8110 8120 8130 8140 8150 8160 8170 8180 8190 8200 8210 8220 8230 8240 8250 8260 8270 8280 8290 8300 8310 8320 8330 8340 8350 8360 8370 8380 8390 8400 8410 8420 8430 8440 8450 8460 8470 8480 8490 8500 8510 8520 8530 8540 8550 8560 8570 8580 8590 8600 8610 8620 8630 8640 8650 8660 8670 8680 8690 8700 8710 8720 8730 8740 8750 8760 8770 8780 8790 8800 8810 8820 8830 8840 8850 8860 8870 8880 8890 8900 8910 8920 8930 8940 8950 8960 8970 8980 8990 9000 9010 9020 9030 9040 9050 9060 9070 9080 9090 9100 9110 9120 9130 9140 9150 9160 9170 9180 9190 9200 9210 9220 9230 9240 9250 9260 9270 9280 9290 9300 9310 9320 9330 9340 9350 9360 9370 9380 9390 9400 9410 9420 9430 9440 9450 9460 9470 9480 9490 9500 9510 9520 9530 9540 9550 9560 9570 9580 9590 9600 9610 9620 9630 9640 9650 9660 9670 9680 9690 9700 9710 9720 9730 9740 9750 9760 9770 9780 9790 9800 9810 9820 9830 9840 9850 9860 9870 9880 9890 9900 9910 9920 9930 9940 9950 9960 9970 9980 9990 10000 10010 10020 10030 10040 10050 10060 10070 10080 10090 10100 10110 10120 10130 10140 10150 10160 10170 10180 10190 10200 10210 10220 10230 10240 10250 10260 10270 10280 10290 10300 10310 10320 10330 10340 10350 10360 10370 10380 10390 10400 10410 10420 10430 10440 10450 10460 10470 10480 10490 10500 10510 10520 10530 10540 10550 10560 10570 10580 10590 10600 10610 10620 10630 10640 10650 10660 10670 10680 10690 10700 10710 10720 10730 10740 10750 10760 10770 10780 10790 10800 10810 10820 10830 10840 10850 10860 10870 10880 10890 10900 10910 10920 10930 10940 10950 10960 10970 10980 10990 11000 11010 11020 11030 11040 11050 11060 11070 11080 11090 11100 11110 11120 11130 11140 11150 11160 11170 11180 11190 11200 11210 11220 11230 11240 11250 11260 11270 11280 11290 11300 11310 11320 11330 11340 11350 11360 11370 11380 11390 11400 11410 11420 11430 11440 11450 11460 11470 11480 11490 11500 11510 11520 11530 11540 11550 11560 11570 11580 11590 11600 11610 11620 11630 11640 11650 11660 11670 11680 11690 11700 11710 11720 11730 11740 11750 11760 11770 11780 11790 11800 11810 11820 11830 11840 11850 11860 11870 11880 11890 11900 11910 11920 11930 11940 11950 11960 11970 11980 11990 12000 12010 12020 12030 12040 12050 12060 12070 12080 12090 12100 12110 12120 12130 12140 12150 12160 12170 12180 12190 12200 12210 12220 12230 12240 12250 12260 12270 12280 12290 12300 12310 12320 12330 12340 12350 12360 12370 12380 12390 12400 12410 12420 12430 12440 12450 12460 12470 12480 12490 12500 12510 12520 12530 12540 12550 12560 12570 12580 12590 12600 12610 12620 12630 12640 12650 12660 12670 12680 12690 12700 12710 12720 12730 12740 12750 12760 12770 12780 12790 12800 12810 12820 12830 12840 12850 12860 12870 12880 12890 12900 12910 12920 12930 12940 12950 12960 12970 12980 12990 13000 13010 13020 13030 13040 13050 13060 13070 13080 13090 13100 13110 13120 13130 13140 13150 13160 13170 13180 13190 13200 13210 13220 13230 13240 13250 13260 13270 13280 13290 13300 13310 13320 13330 13340 13350 13360 13370 13380 13390 13400 13410 13420 13430 13440 13450 13460 13470 13480 13490 13500 13510 13520 13530 13540 13550 13560 13570 13580 13590 13600 13610 13620 13630 13640 13650 13660 13670 13680 13690 13700 13710 13720 13730 13740 13750 13760 13770 13780 13790 13800 13810 13820 13830 13840 13850 13860 13870 13880 13890 13900 13910 13920 13930 13940 13950 13960 13970 13980 13990 14000 14010 14020 14030 14040 14050 14060 14070 14080 14090 14100 14110 14120 14130 14140 14150 14160 14170 14180 14190 14200 14210 14220 14230 14240 14250 14260 14270 14280 14290 14300 14310 14320 14330 14340 14350 14360 14370 14380 14390 14400 14410 14420 14430 14440 14450 14460 14470 14480 14490 14500 14510 14520 14530 14540 14550 14560 14570 14580 14590 14600 14610 14620 14630 14640 14650 14660 14670 14680 14690 14700 14710 14720 14730 14740 14750 14760 14770 14780 14790 14800 14810 14820 14830 14840 14850 14860 14870 14880 14890 14900 14910 14920 14930 14940 14950 14960 14970 14980 14990 15000 15010 15020 15030 15040 15050 15060 15070 15080 15090 15100 15110 15120 15130 15140 15150 15160 15170 15180 15190 15200 15210 15220 15230 15240 15250 15260 15270 15280 15290 15300 15310 15320 15330 15340 15350 15360 15370 15380 15390 15400 15410 15420 15430 15440 15450 15460 15470 15480 15490 15500 15510 15520 15530 15540 15550 15560 15570 15580 15590 15600 15610 15620 15630 15640 15650 15660 15670 15680 15690 15700 15710 15720 15730 15740 15750 15760 15770 15780 15790 15800 15810 15820 15830 15840 15850 15860 15870 15880 15890 15900 15910 15920 15930 15940 15950 15960 15970 15980 15990 16000 16010 16020 16030 16040 16050 16060 16070 16080 16090 16100 16110 16120 16130 16140 16150 16160 16170 16180 16190 16200 16210 16220 16230 16240 16250 16260 16270 16280 16290 16300 16310 16320 16330 16340 16350 16360 16370 16380 16390 16400 16410 16420 16430 16440 16450 16460 16470 16480 16490 16500 16510 16520 16530 16540 16550 16560 16570 16580 16590 16600 16610 16620 16630 16640 16650 16660 16670 16680 16690 16700 16710 16720 16730 16740 16750 16760 16770 16780 16790 16800 16810 16820 16830 16840 16850 16860 16870 16880 16890 16900 16910 16920 16930 16940 16950 16960 16970 16980 16990 17000 17010 17020 17030 17040 17050 17060 17070 17080 17090 17100 17110 17120 17130 17140 17150 17160 17170 17180 17190 17200 17210 17220 17230 17240 17250 17260 17270 17280 17290 17300 17310 17320 17330 17340 17350 17360 17370 17380 17390 17400 17410 17420 17430 17440 17450 17460 17470 17480 17490 17500 17510 17520 17530 17540 17550 17560 17570 17580 17590 17600 17610 17620 17630 17640 17650 17660 17670 17680 17690 17700 17710 17720 17730 17740 17750 17760 17770 17780 17790 17800 17810 17820 17830 17840 17850 17860 17870 17880 17890 17900 17910 17920 17930 17940 17950 17960 17970 17980 17990 18000 18010 18020 18030 18040 18050 18060 18070 18080 18090 18100 18110 18120 18130 18140 18150 18160 18170 18180 18190 18200 18210 18220 18230 18240 18250 18260 18270 18280 18290 18300 18310 18320 18330 18340 18350 18360 18370 18380 18390 18400 18410 18420 18430 18440 18450 18460 18470 18480 18490 18500 18510 18520 18530 18540 18550 18560 18570 18580 18590 18600 18610 18620 18630 18640 18650 18660 18670 18680 18690 18700 18710 18720 18730 18740 18750 18760 18770 18780 18790 18800 18810 18820 18830 18840 18850 18860 18870 18880 18890 18900 18910 18920 18930 18940 18950 18960 18970 18980 18990 19000 19010 19020 19030 19040 19050 19060 19070 19080 19090 19100 19110 19120 19130 19140 19150 19160 19170 19180 19190 19200 19210 19220 19230 19240 19250 19260 19270 19280 19290 19300 19310 19320 19330 19340 19350 19360 19370 19380 19390 19400 19410 19420 19430 19440 19450 19460 19470 19480 19490 19500 19510 19520 19530 19540 19550 19560 19570 19580 19590 19600 19610 19620 19630 19640 19650 19660 19670 19680 19690 19700 19710 19720 19730 19740 19750 19760 19770 19780 19790 19800 19810 19820 19830 19840 19850 19860 19870 19880 19890 19900 19910 19920 19930 19940 19950 19960 19970 19980 19990 20000 20010 20020 20030 20040 20050 20060 20070 20080 20090 20100 20110 20120 20130 20140 20150 20160 20170 20180 20190 20200 20210 20220 20230 20240 20250 20260 20270 20280 20290 20300 20310 20320 20330 20340 20350 20360 20370 20380 20390 20400 20410 20420 20430 20440 20450 20460 20470 20480 20490 20500 20510 20520 20530 20540 20550 20560 20570 20580 20590 20600 20610 20620 20630 20640 20650 20660 20670 20680 20690 20700 20710 20720 20730 20740 20750 20760 20770 20780 20790 20800 20810 20820 20830 20840 20850 20860 20870 20880 20890 20900 20910 20920 20930 20940 20950 20960 20970 20980 20990 21000 21010 21020 21030 21040 21050 21060 21070 21080 21090 21100 21110 21120 21130 21140 21150 21160 21170 21180 21190 21200 21210 21220 21230 21240 21250 21260 21270 21280 21290 21300 21310 21320 21330 21340 21350 21360 21370 21380 21390 21400 21410 21420 21430 21440 21450 21460 21470 21480 21490 21500 21510 21520 21530 21540 21550 21560 21570 21580 21590 21600 21610 21620 21630 21640 21650 21660 21670 21680 21690 21700 21710 21720 21730 21740 21750 21760 21770 21780 21790 21800 21810 21820 21830 21840 21850 21860 21870 21880 21890 21900 21910 21920 21930 21940 21950 21960 21970 21980 21990 22000 22010 22020 22030 22040 22050 22060 22070 22080 22090 22100 22110 22120 22130 22140 22150 22160 22170 22180 22190 22200 22210 22220 222

[illegible]

1130	1140	1150	1160	1170	1180	1190	1200
790	800	810	820	830	840	850	
CAATTTCTCTGTTGTAGTGAAGAGTGGCCCTCTGGAGCCTCCAGGGTGGTGGTGCACATGATGA							
CACAGGGGATTTTGTCTCTAGAGTAAGGCTCATCTGGGCTGGGCCCGCCACCTGGTGGCCCTGTGCTTGA							
1210	1220	1230	1240	1250	1260	1270	
860	870	880	890	900	910	920	
ATGTATGATCGTGTTCCTCCATTACCAAGAGCTTTAAATCCCTCATCTCAGTACACACGGGAGGTCTAGCA							
GGTGAGCCCATGTCCATCTCTGGGCCACTGTGCAGAACCACTTTGGGAGTGTATCCTTACAAACACACAT							
1280	1290	1300	1310	1320	1330	1340	
930	940	950	960	970	980	990	
TTTCTTCATTAGTGTATGCTGTGCCATTATCATGCAACACCTCAGGACTCCTGGATCTCTGCCTAGTTGAGC							
GCCTGGCTCTCCAGAACCACTGTCCAGCTCCAGCTGGAGGATC-----AGGCCCTGGATCCCGGCC--GTTATCC							
1350	1360	1370	1380	1390	1400	1410	
1000	1010	1020	1030	1040	1050	1060	1070
TCCGCACTGCTGCCTCTCTGGGAGGTGAGGAGGCGCCATGTTCAATGGATCTGTGCGAGTTGTAAACA							
ATCTGAGGCTGCAGGCTCTTGGGTGAACAGGACACAGACCCCTCA-----CCTCACAGATTCTCT							
1420	1430	1440	1450	1460	1470		
1080	1090	1100	1110	x			
CATTAGGTGCTTAATAACAGAGCTGTGATGTTAAAAAATAAAAAA							
CACACTGGGGAATAAAGCCATTTCAGAGGAAAAAATAAAAAA							
1480	1490	1500	1510	1520	x		

9. US-09-030-606-177 (1-1119)
US-08-904-809-23 Sequence 23, Application US/08904809

Initial Score	=	68	Optimized Score	=	188	Significance	=	0.65
Residue Identity	=	29%	Matches	=	208	Mismatches	=	484
Gaps	=	7	Conservative Substitutions	=	0			

x	10	20					
CGCCACTCGCAGCCCTGGCAGG							
CNANAGANAATCCNCTGCCTTCCANAGTANACNATTTGAACNNGAGAACCCNGGCGAATCGTAATNAGG							
130	140	150	160	170	180	190	
30	40	50	60	70	80	90	
CG-GCACTGCTATGGAARACGAATGTTCTGCTCGGGCGTCT--GGTGCATCCGAGTGGGTGCTGTCTG							
CGTGCGCCGCAATNTGTNCGGTTTATTNTCCAGCTNCCTNCCNACCTACNTCTTCNNAGCTGTCTNN							
200	210	220	230	240	250	260	270
100	110	120	130	140	150	160	
CGGCACACTGTTTCCAGACTCTACACATCGGGCTGGGCTGTCACAGTCTTTAGGCGCCACCAAGACGAC							
ACCCCTTNGCNACCCCNAGGTCGGATCGGGTTNNNTGACCGNGCNCCTCCGCCNTTCCATNA							
280	290	300	310	320	330	340	
170	180	190	200	210	220	230	
GGAGCCAGATGGTGGGCGCAGCTCTCCGTACGGCACCCAGAGTACAACAGACCCCTTGTCTGCTAACGACC							
CGANCCNCCGACCAACCNANCGNCGCCGNNCTCTTCGCCNCCCTGTCTNTNCCCTGTNGCCCTGG							
350	360	370	380	390	400	410	
240	250	260	270	280	290	300	
TCATGCTCATCAAGTTGGAGGAATCCGTGTCCGAGTCTGACACCATCCGGAGCATCAGATTGCTTCGCGAT							
CNMGNACCGGATTGACCTCGCCNCTNCNNGAAACNGANACGTCCGGGTGTNNANNANCCTGTGGGNN							
420	430	440	450	460	470	480	
310	320	330	340	350	360	370	
GCCCTTACCGGGGAACCTGTGCTCGTTCTGGCTGGGTCTGCTGGCAACGATCTGTGATTGCCATCC							


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NGCGTGTGCNCCGGTTCCTCCNNCCNCTTCCACCATCTTCNTTACNGGCTCTCCNCGCCNCTCTNNNCAC
490 500 510 520 530 540 550
380
AGTCCCAGACTGTGGAGGCTGGAGTGTGAGAAGCTTCCCAACCCCTGGCAGGTTGTACCAATTCGGCAA
410 420 430 440 450
|||||
NCCCTGGGACGCTATCTCTNTGCCCCCTTNACTCCGCCCTTCGNCGTGNCGCCGCCACCACTCATTTNCA
560 570 580 590 600 610 620 630
|||||
CTTCCAGTGAAGGACGCTCTGTGCTGCTCACTCTCACTGCTGCTCACTGCTCACTCACCACCGGAACAC
460 470 480 490 500 510 520
|||||
NACGNTCTTCAAAANNCTCGTNNCTCCNANCNNGNCNCTCANCCNAGGGAAGGNGGNNCCNNTGNT
640 650 660 670 680 690 700
530 540 550 560 570 580 590
TGATGTAACCTAGCAGCACCATAGTTCTCCGAAGTCAGACTATCATGATTACTGTGTGACTGTGTGTCT
710 720 730 740 750 760 770
|||||
TGAGCTTGGNGANGTCCGAANANTCTCNCNCTCANCNCTACC---CCTCGGGCGNCTCTCNGTNNCCA
780 790 800 810 820 830 840
600 610 620 630 640 650 660
ATTGCTACTAACCATGCGCATGTTTGTAGTGAATTAAGGTCACTTGGGCTC-AACCATCTTGTGTATCCAGTTA
780 790 800 810 820 830 840
ACTTANCAANTCTCCCGGNGGNCNCTCTCAGGCTCNCCNCCNCTCTCTGCANTGNTCTGTGCTTNA
850 860 870 880 890 900 910
670 680 690 700 710 720 730
TCCCTACTGAATGAGATTTCTCTGCTCAGTGTGAGCATTCGCCATTAATTTCTGACCTACAGAGGTGAGG
850 860 870 880 890 900 910
CCNNTACGANTTTCGNCNCCCTCTTCC
870 880 890 900 910
740
GATCAT
740
10. US-09-030-606-177 (1-1119)
US-08-904-809-8 Sequence 8, Application US/08904809
Initial Score = 64 Optimized Score = 243 Significance = 0.58
Residue Identity = 34% Matches = 279 Mismatches = 512
Gaps = 28 Conservative Substitutions = 0
210 220 230 240 250 260 270
GAGTACAACAGACCCCTGCTCGCTAAGCACCTCATGCTCATCAAGTTGGACGAATCCGCTGCCAGTCTGAC
|||||
CATTTCCGGGTTTACTTTCTAA
X 10 20
280 290 300 310 320 330 340
ACCATCCGGAGCATCAGC--ATTGCTTGCAGTGCCTTACCGCGGGAACCTTGCCTCTGTTCTGGCTGGG
|||||
GGAACCGGACGGAAGCTGTACGTGGGAATCGGTGCATAGGAGAACCTTCTGCTGGCAGCGCTAGGG
30 40 50 60 70 80 90
350 360 370 380 390 400 410
GTCTGTGCGGAAGAGATGCTGTGATGTCATCCAGTCCAGACTGTGGAGGCTGGGAGTGTGAGAAGCTTT
|||||
ACAAGCGGAGAGGAGCTCCGAGGCTGTGAAGCGCACGTCCCAAGAGTGGACCTTGGCACTGAACACGCTGG
100 110 120 130 140 150 160
420 430 440 450 460 470 480 490
CCCAACCTCGCAGGAGTGTACCAATTTTCGGAACCTTCCAGTGCAGGACGCTCTGCTCATCTCCACTGGGT
|||||
GACA--CATCCGCGAGTACGAACGCGCTGAAGTGTGGAGCGGAGGTCCAGCAGTGTGCGCGCTCT
170 180 190 200 210 220 230
500 510 520 530 540 550 560
GCTCACTACTGCTCACTGCAATCCCGGAACACTGTGATCAACTAGCAGCAGCACCATAGTTCTCCGAAGTCAG
|||||
GGGTGGGTGGCGANGCCCTGACCC-----GCTCTGCTGCTGTGCTGCCCCANGTGGCGGCCACCC
240 250 260 270 280 290

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570 580 590 600 610 620 630
ACTATCATGATTACTGTGCTGACTGTGCTGTATTTACTTAACCATCCGATGCTTTAGGTGAATTTAGCGT
|||||
CTGACCTGCTTGGTCCAAACACTGAGCCCTGCTGGCGGACTTCAAGGANAAACCCACACANGGGATTTCG
300 310 320 330 340 350 360
640 650 660 670 680 690 700
CACTTGGGCTCAAGCATCTTGTGATCCAGTTATCTCACTGAATTTAGATTTCCTGCTTCAAGTGC----AG
|||||
TCCATANANTAGGCTCATCTCGGCTCGGCCCCCACTGCTGGCCCTGCTCTTTTGANGTGAGCCCCCATGT
370 380 390 400 410 420 430 440
710 720 730 740 750 760 770
CCATTTCGCACATAATTTCTGACCTACAGAGGTGAGGATCATATAGCTCTTCAAGAGTCTGGTACTCCCTT
|||||
CCATCTGGCCACTGTGNGACCACTTTNGGAGTGTCTCTTACAAACACANNATGCCCGGCTCTCC
450 460 470 480 490 500 510
780 790 800 810 820 830 840
CACAAATTCATTTCTCTCTGTTGTAGTGAAGGTGCGCCCTCTGGAGCCTCCAGGTTGGTGTGCAAGTCA
|||||
GGAACCACTCCCAACCTG-----NGAAGGATCAAGNCCTGNATCCACTNNTNCTANAAACCGGCCNCC
520 530 540 550 560 570
850 860 870 880 890 900 910
AATGATGAATCTATGATGCTGCTTCCCACTTACCCAAAGCTTTAAATCCCTCATGCTCAGTACACAGGCG
|||||
CGNGTGAACCCNCCCTTCTCTTCTTCTTNTNAGGTTAATNNGCCTTGGCCCTTNCANNGTCCCTNCC
580 590 600 610 620 630 640 650
920 930 940 950 960 970 980
GTCTAGCATTTCTTCTTCTTCTGATGCTGTCTCCATTTATGCAAC--CACCTCAGGACTCTCTGGATCTCTG
|||||
NTTTCCNNTGTTNAAATTTGTANGCNCNCCNNTTCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC
560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720
990 1000 1010 1020 1030 1040 1050 1060
CTAGTTGAGCTCTCTGATGCTGCTCTCTCTTGGGAGGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG
|||||
CTGGGTGTCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCCNCC
730 740 750 760 770 780 790
X 1070 1080 1090 1100 1110
AGTTGTACACATTAGTGTCTTAATAAACAAGAGTGTGTGTTAAAAA
|||||
ANNCG
X

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11. US-09-030-606-177 (1-1119)

US-09-020-747-8 Sequence 8, Application US/09020747

Initial Score = 64 Optimized Score = 243 Significance = 0.58
Residue Identity = 34% Matches = 279 Mismatches = 512
Gaps = 28 Conservative Substitutions = 0

```

210 220 230 240 250 260 270
GAGTACAACAGACCCCTGCTCGCTAAGCACCTCATGCTCATCAAGTTGGACGAATCCGCTGCCAGTCTGAC
|||||
CATTTCCGGGTTTACTTTCTAA
X 10 20
280 290 300 310 320 330 340
ACCATCCGGAGCATCAGC--ATTGCTTGCAGTGCCTTACCGCGGGAACCTTGCCTCTGTTCTGGCTGGG
|||||
GGAACCGGACGGAAGCTGTACGTGGGAATCGGTGCATAGGAGAACCTTCTGCTGGCAGCGCTAGGG
30 40 50 60 70 80 90
350 360 370 380 390 400 410
GTCTGTGCGGAAGAGATGCTGTGATGTCATCCAGTCCAGACTGTGGAGGCTGGGAGTGTGAGAAGCTTT
|||||
ACAAGCGGAGGAGGAGCTCCGAGGCTGTGAAGCGCACGTCCCAAGAGTGGACCTTGGCACTGAACACGCTGG
240 250 260 270 280 290

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380 X
TTTT
GGGATCCCAACAATCAGGTCCTCCCTGAGATAGCTGCTGATGGCTGATCATTTG
1510 X 1520 1530 1540 1550 1560

14. US-09-030-606-223' (1-383)
US-08-850-713-16 Sequence 16, Application US/08850713

Initial Score = 51 Optimized Score = 133 Significance = 2.13
Residue Identity = 36% Matches = 144 Mismatches = 233
Gaps = 9 Conservative Substitutions = 0

X 10 20
TTTTAAACATATAGCTTAATGG
|||||
GGCTCAGGTTAAACAGTACGCTAGCTCCCTGAGATAGCTGCTGATGGCTGATCATTTG
1090 1100 1110 1120 1130 X 1140 1150
|||||
TCAAAACAAGTCAATAAAGATTAATTTACAAGTATCAGAAGTGAAGACTGTGGTCTCTATAACTNTTCCC
|||||
AGTCACCTGTTTCCCATCTCTAAGCCCTTAACCTGCAGCTTCGTTTAATGTAGCTCTTGCAATGGAGTTT
1160 1170 1180 1190 1200 1210 1220
|||||
CCACCAAGTTAAATATAATTTGTCTAGCTTCCCTGGCAGCATTTACTTTTGATAAGAAGTCTCCAAATAAATA
1230 1240 1250 1260 1270 1280 1290
|||||
CTAGGATGAACACACTCTCTCCATGGATTTGAACATATGAAGTATTTGTAGGGAAGAGTCTCTGA-----
1300 1310 1320 1330 1340 1350 1360
|||||
170 180 190 200 210 220 230
AKGGAAACACTACTAATCTCTAGACTTCCCTGGCAGCATTTACTTTTGATAAGAAGTCTCCAAATAAATA
1370 1380 1390 1400 1410 1420 1430
|||||
GGGCAACACAGAAGACAGGTCCTCCCTAGCCCAAGACAGCTGCTTTTGGTCTGACCCCTCCCTTACC
1440 1450 1460 1470 1480 1490 1500
|||||

240 250 260 270 280 290 300 310
CAAAATTTGGCAGACATTTAATCTGTCAAGACAATGTAAAGAAATGCCCCAMAAYAYWATTAATTTG
|||||
TTTTATCAGGATGGCTGTGTGCTCTCTGTGTCATCAGACAGACAGCATTTAAATATTAAACITA
1370 1380 1390 1400 1410 1420 1430
|||||
320 330 340 350 360 370
ACCAATATACCAATATCAG---TCCCTAAGATAATTTCTGAATGAAGAATTTGTTTTTGTGTTTGT
|||||
TTTTATTAACAAGTGAAGGAATCCATTCGATGCTTTCTGTGTTGGTGTCTAATATTGGGTAGGTTGG
1440 1450 1460 1470 1480 1490 1500
|||||

380 X
TTTT
GGGATCCCAACAATCAGGTCCTCCCTGAGATAGCTGCTGATGGCTGATCATTTG
1510 1520 1530 1540 1550 1560

15. US-09-030-606-223' (1-383)
US-08-904-809-53 Sequence 53, Application US/08904809

Initial Score = 50 Optimized Score = 137 Significance = 2.05
Residue Identity = 38% Matches = 153 Mismatches = 230
Gaps = 9 Conservative Substitutions = 0

X 10 20 30
TTTTAAACATATAGCTTAATGTGTCAAAACAAGT
|||||
ACATAATTTACAGGGCTAATACCAATGAAGTGTCTATTATTAAAGGTTATGATCTGAGTATTACAGTT
10 20 30 40 50 60 70
|||||
40 50 60 70 80 90 100
GCAATAAAGATTAATTTACAAGTATCAGAAGTGAAGACTGTGCTCTATAACTNTTCCCCACCAAGTT
|||||

GCTGAAGTTTGGTATTTTATCCAGCATTTCTTTTGTGTTGATAACACTACACAACCCITAAAGACACTG
80 90 100 110 120 130 140
|||||
110 120 130 140 150 160 170
AAAATATAATTTGCTCATTCAGGAAATCAA---ATCTTTTAGAATAGCAGCACTCCCAACAGTGAAGGAA
|||||
AAAATTAAGTAAAGTTCAGAACATTAAGTGTCTCAATCAATCTCTACATACACTATATAGTAAATPAAA
150 160 170 180 190 200 210
|||||
C---ACTACTACTTCTTAGACTTCTCTTTGGCAGCATTTACTTTTGATAAGAAGTCTCCAAATAAATAACAAA
180 190 200 210 220 230 240
|||||
CGTTAAAAAAGTGTGGAATCTGCAGTATATANACCGCTCTCTGAGGATAANACTGCTTTGGACAGAGA
220 230 240 250 260 270 280
|||||
250 260 270 280 290 300 310
ATTTTGGCAGACATTTAAATCTTGTCAAGCAATGTAAAGAAATGCCCCAMAAYAYWATTAATTTGACC-
|||||
AAGGAAAAAAGCTTTGANTTTCTTTGCTGATANGAGGAAGGCTGAATTACCTTGTTCCTCTCCCT
320 330 340 350 360
-ATAATTTACCAATATCAGTCCCTCAAGATAATTTCTGAATGAAGAATTTGTTTTTGTGTTGTTTT
|||||
AATGATTGGCAGGTGNGGTAATNCCAAACATATTCCAACTCAACACTTCTTTCCNCGTANCITGANTCT
370 380 390 400 410 420 430
|||||
GTGTATTTCCAGGANCAGGCGGATGGAATGGCCAGCCNCGGATGTTCC
440 450 460 470 480
|||||

16. US-09-030-606-223' (1-383)
US-09-020-747-53 Sequence 53, Application US/09020747

Initial Score = 50 Optimized Score = 137 Significance = 2.05
Residue Identity = 38% Matches = 153 Mismatches = 230
Gaps = 9 Conservative Substitutions = 0

X 10 20 30
TTTTAAACATATAGCTTAATGGTCAAAACAAGT
|||||
ACATAATTTAGCAGGCTAATTAACATAAGATGCTATTATTAAAGGTTATGATCTGAGTATTAAACAGTT
10 20 30 40 50 60 70
|||||
40 50 60 70 80 90 100
GCAATAAAGATTAATTTACAAGATATCAGAAGTGAAGACTGTGCTCTATAACTNTTCCCCACCAAGTT
|||||
GCTGAAGTTTGGTATTTTATGCGAGCATTTCTCTTTTGTGATAACACTACAGAACCCCTTAAGGACACTG
80 90 100 110 120 130 140
|||||
110 120 130 140 150 160 170
AAAATATAATTTGCTCATTCAGGAAATCAA---ATCTTTTAGAATAGCAGCACTCCCAACAGTGAAGGAA
|||||
AAAATAGTAAAGTAAAGTTTCAAGAACATTAAGTGTCTCAATCAATCTCTACATAACACTATAGTAAATPAAA
150 160 170 180 190 200 210
|||||

180 190 200 210 220 230 240
C---ACTACTAATTCCTTAGACTTCTCTTTGGCAGCATTTACTTTTGATAAGAAGTCTCCCAATAAATACAAA
|||||
CGTTAAAAAAGTGTGGAATCTGCACTAGTATANACCGCTCTCTGTCAGGATAANACTCTCTTTGGACAGAGA
220 230 240 250 260 270 280
|||||
250 260 270 280 290 300 310
ATTTTGGCAGACATTTAATCTGTCAAGACAATGTAAAGAAATGCCCCAMAAYAYWATTAATTTGACC-
|||||
AAGGAAAAAAGCTTTGANTTTCTTTGCTGATANGAGGAAGGCTGAATTACCTTGTTCCTCTCCCT
290 300 310 320 330 340 350 360
|||||

320 330 340 350 360 370 380 X
-ATAATTTACCAATATCAGTCCCTCAAGATAATTTTCTGAATGAAGAATTTGTTTTTGTGTTGTTTT
|||||
AATGATTGGCAGGTGNGGTAATNCCAAACATATTCCAACTCAACACTTCTTTTCCNCGTANCITGANTCT
370 380 390 400 410 420 430
|||||

[illegible]

GTTCCCMTCATTTGTTGGAGTGTCTATCTTAAAGATTTTGAATTCCTCGAATACAAATATATATTAA
 TTTCCCAATCGCTAATTTCCAACAACAACAATAACATGTTTGGCTGTTTNNAGTTGTATAAAGATNGCT
 TTTGGTGGGGAANAGTTATAGGACCACAGTCTTCACATCTGTGATACITGTAAATATCTTTATGCGACT
 GATCTCTGTTATNAAAGAAATATTTC-----TGTGATACATACGTCTGCAANTCTGTATTTATGTCGTC
 290 300 310 320 330 340 350
 220 230 240 250 260 270 280

2. US-09-030-000-223 (1-385)
US-09-020-747-11 Sequence 116, Application US/09020747

2. Conservative substitutions

AAACAACAACAACAACAACAATCTCTTCATTCACAAAAATATCTTAGGCACGATATGGTAAATATGG
 10 20 30 40 50 60 70
 ACAGGATATAGTGTGTTNAGTTATTGTTNATGTTAAATACAT
 x 10 20 30 40

TCATTTAAATWRTTITKGGGGATTTCCTTACATTGTCTTGACATAGATTAAATCTGTGCCAAAATTTT
 |||||
 TGAATTTCTGTATACCTCTGATTACACATTATCCCTTTAAAGAGATGAATCTTAATTTTATGCCCAT
 50 60 70 80 90 100 110 120 130 140

150 160 170 180 190 200 210
GTATTTTATTGGAGACTCTTATCAAAAGTAATGCTGCCAAGGAAGTCTAAGGAATTAGTAGTGTTCCCM
|||||
CTATTAATTTACCAATAGTACCTGTTAAATGAGAGCAATCATGATAGCACTGAATTTTAACTAGTAGTTTGACT
130 140 150 160 170 180 190 200 210

220 230 240 250 260 270
 TCACGTGTTGGAGTGCTATTCTAAAGATTTTGATTCTCTGGATGACAAATATATTTT
 || || ||
 TCTAAGATTGGT 190 x

3. US-09-030-606-223 (1-383)
US-09-020-747-93 Sequence 93, Application US/09020747

5. US-09-030-606-223 (1-383)
US-09-020-747-58 Sequence 58, Application US/09020747

Pair Score	2	Openand Score	81	Mismatches	117
Indel Identity	408	Matches	81	Mismatches	117
s	0	Conservative Substitutions	0		

TCACATTTAAATTTTCTTTGGGGCATTTTCCCTTACATGTCCTCTTGGACAGATTTAAATGTCGTGCGCCAAAATTTTTC

TGAATTTTCTGTATACCTCTGATACATACATTTATCCTTTTAAAAAGAGTAAATCTCTTAATTTTATGCGCA
 50 60 70 80 90 100 110
 150 160 170 180 190 200 210
 CTATTTTATTTTGGACATCTCTTTATCAAAAGTAATGCTGCCAAAGGAATCTAAGGAATAGTAGTATGCTCCG

CTATTAAATTTACCAATGAGTTACCTTGTTAAATGAGAAGTCATGATAGCACTGAATTTTAACTAGTTTGTGACT


```

100 110 120 130 140 150 160
GCATTTCTTACATGCTTGAAGAATAAAT-GTCTGTGCAAAATTTTGTATTTATTTGGAGCTTC
|||||
ACATCTGCAAACTTCTTCTCAATTTCTGGCCAATCATCCATGCTCATCTGATTTGGGAAGTTCATCAGACTTT
210 220 230 240 250 260 270
ACCTGGCGGTTACCAACTTAATCGCTTGCAGCACATCCCTTTTCGCCAGC
X 500 510 520 530 540

170 180 190 200 210 220 230
TTATCAAAAGTAATGTCGCAAGGAGTCTAAGGAATTAGTAGTCTTCCMTCACTGTTTGGAGTGTGCT
|||
AGTCCANNCTTTGATCAGCAGCTCTAGAACCTGGGTTCTATTGCTCCAACAGCATGAATTTCCCATCT
280 290 300 310 320 330 340
ATTCTAAAGATTTGATTTCCGGAATGACAATTAATTTTAACCTTGTGGGGAAANAGTTATAGGACC
240 250 260 270 280 290 300
GCCTGCTGTAAGTCGTATAGAAAGGTGCTCCACCATCAACATGTTCTGCTCGAGGGGGGCCCGGTAC
350 360 370 380 390 400 410 420
310 320 330 340 350 360 370 380
ACAGCTTTCACCTCTGATCTTGTAAATTAATCTTTTATGCACTTGTTTGACCATTAAAGCTATATGTTTA
|||
CCAATTCGCCCTATANTAGTCGTATATACGCGGCTCACTGCGCTGCTTTTACAACGCTGTCGACTGGGAAA
430 440 445 450 460 470 480 490
X
AAA
ACCTGGCGGTTACCAACTTAATCGCTTGCAGCACATCCCTTTTCGCCAGC
X 500 510 520 530 540
```

16. US-09-030-606-223 (1-383)

US-08-904-809-3 Sequence 3, Application US/08904809

Initial Score = 47 Optimized Score = 129 Significance = 1.99
Residue Identity = 35% Matches = 138 Mismatches = 245
Gaps = 2 Conservative Substitutions = 0

```

70 80 90 100 110 120 130
TCCTGCTCTCACTGCTGATGAAGAGCCCGTCTCTGTTGTGATCATGATGAACAACCTCTCAAAAGTC
70 80 90 100 110 120 130
AATCTCTCACTCAGAAAATATCTTAGGACTGATATGGTAATTA-TGGTCAATTTAATWTRTKTGGG
|||
AGAACGGAGTCACAGGCACTGTGCCGTCAAGATTTGACACCACCTGCTCTGCTCTTTTGGCAAT
140 150 160 170 180 190 200
100 110 120 130 140 150 160
GCATTTCTTACATGCTTGAAGAATAAAT-GTCTGTGCAAAATTTTGTATTTATTTGGAGACTTC
|||||
ACATCTGCAAACTTCTTCTCAATTTCTGGCCAATCATCCATGCTCATCTGATTTGGGAAGTTCATCAGACTTT
210 220 230 240 250 260 270
280 290 300 310 320 330 340
TTATCAAAAGTAATGTCGCAAGGAGTCTAAGGAATTAGTAGTCTTCCMTCACTGTTTGGAGTGTGCT
|||
AGTCCANNCTTTGATCAGCAGCTCTAGAACCTGGGTTCTATTGCTCCAACAGCATGAATTTCCCATCT
280 290 300 310 320 330 340
240 250 260 270 280 290 300
ATTCTAAAGATTTGATTTCCGGAATGACAATTAATTTTAACCTTGTGGGGAAANAGTTATAGGACC
|||
GCTGTCTCTGTAAGTCGTATAGAAAGGTGCTCCACCATCAACATGTTCTGCTCGAGGGGGGCCCGGTAC
350 360 370 380 390 400 410 420
170 180 190 200 210 220 230
TTATCAAAAGTAATGTCGCAAGGAGTCTAAGGAATTAGTAGTCTTCCMTCACTGTTTGGAGTGTGCT
|||
AGTCCANNCTTTGATCAGCAGCTCTAGAACCTGGGTTCTATTGCTCCAACAGCATGAATTTCCCATCT
280 290 300 310 320 330 340
240 250 260 270 280 290 300
ATTCTAAAGATTTGATTTCCGGAATGACAATTAATTTTAACCTTGTGGGGAAANAGTTATAGGACC
|||
GCTGTCTCTGTAAGTCGTATAGAAAGGTGCTCCACCATCAACATGTTCTGCTCGAGGGGGGCCCGGTAC
350 360 370 380 390 400 410 420
310 320 330 340 350 360 370 380
ACAGCTTTCACCTCTGATCTTGTAAATTAATCTTTTATGCACTTGTTTGACCATTAAAGCTATATGTTTA
|||
CCAATTCGCCCTATANTAGTCGTATATACGCGGCTCACTGCGCTGCTTTTACAACGCTGTCGACTGGGAAA
430 440 445 450 460 470 480 490
X
AAA
ACCTGGCGGTTACCAACTTAATCGCTTGCAGCACATCCCTTTTCGCCAGC
X 500 510 520 530 540
```

```

430 440 450 460 470 480 490
X
AAA
ACCTGGCGGTTACCAACTTAATCGCTTGCAGCACATCCCTTTTCGCCAGC
X 500 510 520 530 540
```

17. US-09-030-606-223 (1-383)

US-09-020-747-3 Sequence 3, Application US/09020747

Initial Score = 47 Optimized Score = 129 Significance = 1.99
Residue Identity = 35% Matches = 138 Mismatches = 245
Gaps = 2 Conservative Substitutions = 0

```

70 80 90 100 110 120 130
TCCTGCTCTCACTGCTGATGAAGAGCCCGTCTCTGTTGTGATCATGATGAACAACCTCTCAAAAGTC
70 80 90 100 110 120 130
AATCTCTCACTCAGAAAATATCTTAGGACTGATATGGTAATTA-TGGTCAATTTAATWTRTKTGGG
|||
AGAACGGAGTCACAGGCACTGTGCCGTCAAGATTTGACACCACCTGCTCTGCTCTTTTGGCAAT
140 150 160 170 180 190 200
100 110 120 130 140 150 160
GCATTTCTTACATGCTTGAAGAATAAAT-GTCTGTGCAAAATTTTGTATTTATTTGGAGACTTC
|||||
ACATCTGCAAACTTCTTCTCAATTTCTGGCCAATCATCCATGCTCATCTGATTTGGGAAGTTCATCAGACTTT
210 220 230 240 250 260 270
170 180 190 200 210 220 230
TTATCAAAAGTAATGTCGCAAGGAGTCTAAGGAATTAGTAGTCTTCCMTCACTGTTTGGAGTGTGCT
|||
AGTCCANNCTTTGATCAGCAGCTCTAGAACCTGGGTTCTATTGCTCCAACAGCATGAATTTCCCATCT
280 290 300 310 320 330 340
240 250 260 270 280 290 300
ATTCTAAAGATTTGATTTCCGGAATGACAATTAATTTTAACCTTGTGGGGAAANAGTTATAGGACC
|||
GCTGTCTCTGTAAGTCGTATAGAAAGGTGCTCCACCATCAACATGTTCTGCTCGAGGGGGGCCCGGTAC
350 360 370 380 390 400 410 420
310 320 330 340 350 360 370 380
ACAGCTTTCACCTCTGATCTTGTAAATTAATCTTTTATGCACTTGTTTGACCATTAAAGCTATATGTTTA
|||
CCAATTCGCCCTATANTAGTCGTATATACGCGGCTCACTGCGCTGCTTTTACAACGCTGTCGACTGGGAAA
430 440 445 450 460 470 480 490
X
AAA
ACCTGGCGGTTACCAACTTAATCGCTTGCAGCACATCCCTTTTCGCCAGC
X 500 510 520 530 540
```

18. US-09-030-606-223 (1-383)

US-08-904-809-46 Sequence 46, Application US/08904809

Initial Score = 45 Optimized Score = 142 Significance = 1.82
Residue Identity = 38% Matches = 154 Mismatches = 229
Gaps = 8 Conservative Substitutions = 0

```

X
AAA
ACCTGGCGGTTACCAACTTAATCGCTTGCAGCACATCCCTTTTCGCCAGC
X 500 510 520 530 540

X
AAA
ACCTGGCGGTTACCAACTTAATCGCTTGCAGCACATCCCTTTTCGCCAGC
X 500 510 520 530 540
```


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$$\begin{array}{ccc} \vee & \text{O} & \vee \\ & \text{---} & \\ \text{O} & & \text{O} \\ & \text{---} & \\ \wedge & \text{O} & \wedge \end{array}$$

FastDB - Fast Pairwise Comparison of Sequences Release 5.4

Results file us-09-030-606-177-inv.res made by tport on Thu 1 May 103 15:08:41-PDT.

Query sequence being compared:US-09-030-606-177' (1-1119)
 Number of sequences searched: 410
 Number of scores above cutoff: 410

Results of the initial comparison of US-09-030-606-177' (1-1119) with:

```
File : 6130043.seq
File : 6252047.seq
File : US08806596.seq
File : US08850713.seq
File : US08904809.seq
File : US09020747.seq
File : US09841894A.seq
```

Scatter plot showing the number of sequences for various amino acids. The y-axis is labeled 'NUMBER' and ranges from 0 to 100. The x-axis is labeled 'SEQUENCES' and lists amino acids: N, U, M, B, E, R, O, F, S, E, Q, U, E, N, C, E, S. Asterisks represent data points. The distribution shows a peak for 'B' (around 45) and 'E' (around 40), with 'S' and 'Q' having the highest counts (around 60).

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Frame
1. US-08-806-596-37	*** 3 standard deviations above mean	760	69	239	3.14
2. US-08-904-809-37	*** 2 standard deviations above mean	760	67	239	2.98
3. US-09-020-747-10	Sequence 106, Application	473	64	158	2.74
4. US-08-806-596-39	Sequence 39, Application	751	60	217	2.43
5. US-08-904-809-39	Sequence 39, Application	751	60	217	2.43
6. US-09-020-747-39	Sequence 39, Application	751	60	217	2.43
7. US-09-020-747-17	Sequence 177, Application	1119	60	148	2.43
8. US-08-904-809-40	Sequence 40, Application	753	58	234	2.27
9. US-09-020-747-11	Sequence 110, Application	3410	56	372	2.12
10. US-09-020-747-79	Sequence 79, Application	552	55	176	2.04
11. US-09-071-710-12	*** 1 standard deviation above mean	294	54	89	1.96
12. US-09-525-397-12	Sequence 12, Application	294	54	89	1.96
13. US-09-020-747-13	Sequence 139, Application	332	54	114	1.96
14. US-09-020-747-69	Sequence 69, Application	536	54	179	1.96
15. US-08-904-809-74	Sequence 74, Application	537	54	174	1.96
16. US-09-020-747-74	Sequence 74, Application	537	54	174	1.96
17. US-08-806-596-32	Sequence 32, Application	789	54	242	1.96
18. US-08-904-809-32	Sequence 32, Application	789	54	242	1.96
19. US-09-020-747-32	Sequence 32, Application	789	54	242	1.96
20. US-09-020-747-14	Sequence 145, Application	303	53	103	1.88

1. US-09-030-606-177' (1-1119)
US-08-806-596-37 Sequence 37, Application US/08806596

Initial Score	-	69	Optimized Score	-	239	Significance	-	3.14
Residue Identity	-	36%	Matches	-	284	Mismatches	-	462
Gaps	-	27	Conservative Substitutions	-	0		-	0

[illegible]

TCCAGAGGCGCCACCTTTCACTACACAGGAGAAATGAATTTGGA--GGGAGTACAGCATCTCTGGAAGA
100 110 120 130 140 150 160
AAGAAACGCTTTAGACACACTGTACAATTTATAATGTAAGTGCCATTTATTGAGTAATATATCTCCCAAGA
170 180 190 200 210 220
GCTATATGATCCCTCACCTCTGTAGGTGAGAAATATGTTGGGATGGCTGACATGAGCAGGAGAAATCTCAA
230 240 250 260 270 280 290
GTGATGTGCTCCCTTCTCCCAACCACTAATGAA-----CAGCAACATTAATTTAATTTATTA
300 310 320 330 340 350
TTCAGTGAAGGATACTACCAAGATGGTTGAGGCCAAGTACGCTTAATTTCCACCTAAACATCGGCATGG
360 370 380 390 400 410 420 430 440
GTAGATATACACTGCTGCAACAGCTAATTCCTTCATCCCATCCCATGTGATATGTTGATATGTTGAGTTG
450 460 470 480 490 500 510
TTAG--TACAATAGACAGCAGTCAACACAGTAAATCATGATATGATCTGACTTCGGAGAACTATGGTGTGGC
520 530 540 550 560 570 580
GTAGAATGCATCACTACAATCAACAGCAAGATGAAGCTAGGCTG-----GGCTTTGG
590 600 610 620 630 640 650
TAGTTGATACACAGTGTTCGGGTGATGACGATGAGCAGTGTGAGCACCAGTGTGAGGATGACAGGAGCTCC
660 670 680 690 700 710 720
TGAAATAGACTGTGTCTGTGAATCAATGATCTGACCTATCTCGGTGGCAAGAACTCTTGAACCGCT
730 740 750
TTGCACGTGGAAAGTTCGCCGAATGTGTACAACTGTCAGGGTTGGGAAAGCTTCTCACACTCCAGCCTCCCA
760 770 780 790 800 810 820 830 840 850
TCCTCAAAGGCGCTGCCACATTTGTGGCTCTTTGACCTGTTTCAAAA
860 870 880 890 900 910 920
CAGTCTGGGACTGGATGCCAATACA

4. US-09-030-606-177' (1-1119)
US-08-806-596-39 Sequence 39, Application US/08806596

Initial Score = 60 Optimized Score = 217 Significance = 2.43
Residue Identity = 30% Matches = 233 Mismatches = 513
Gaps = 9 Conservative Substitutions = 0

140 150 160 170 180 190 200 210
TCCAGGAGCTCTGAGGTGGTTGTCATGAATGGACAGCATACACTAAATGAAGAAATGCTAGACCTGCCCTGGT
220 230 240 250 260 270 280
GTACTGACATGAGGATTTAAAGCTTTGGTAAATGGAAACACAGCATCATCATTCATTCATGACCTGCA
290 300 310 320 330 340 350
CACATTTAATTTTATTTGATTTTAAATGCTGTCACAAACAATATTTATTCATTTGTTCTTTTAT
360 370 380 390 400 410 420
CAGCATCTTGAAGAGCTPATATGATCCCTCACCTGTAGTCAAGAGAAATGTTGGGAAATGCTGACACTGA
430 440 450 460 470 480 490
AGCAGGAAATCTCAATTCAGTGAGGATAACTGGATACCAAGATGGTTGAGGCCAAGTACGCTAATTTCCAC

TTCCGAAATCACTCGGGGGAAGAAAGTTGCTTTCTTAATCATGCCCTATGCTGGTGTATTAACCTGCTT
240 250 260 270 280 290 300
500 510 520 530 540 550 560 570
TAAACATCGGATGTTAGTACAATAGACACAGTCAACACAGTAAATCATGATACATCTGACTTCGGAGAA
580 590 600 610 620 630 640
GTACAATTAACCTTTACATTTTAATTAATGCTNAANGCTTTAATTANACTTGGGGGTTCCCTCCCCANAC
650 660 670 680 690 700 710
CTATGGTCTGCTGCTAGTATGATCACATGCTTCGGGTGATGAGTGCAGTGCAGTAGTGTGCACCCAGTGGATG
720 730 740 750 760 770 780
CAACCCNCTGACAAAAGTCCNGCCCTCAAAATATGTCGGGNNCTNTTGAACACACANGCNGAANGTT
790 800 810 820 830 840 850
CAGCAGGAGCTCTTGCACTGGAAGTTGCG-----AAATGGTACAACCTGCCAGGTTGGGAAAGTTCT
860 870 880 890 900 910 920
CTCATTTNCCCNCCAGGTAATAATGAAGGTTACCATTTTAAACCCACTCCACATGGCANNNGCTGA
930 940 950 960 970 980
CACACTCCAGCCTCCCACTGCTGGGACTGGATGGCAATCACAGCATGCTTCGCCACAGCAGCCAGCCAG
990 1000 1010 1020 1030 1040 1050
ATCCTCNAAAANCCNCCCTCAANNAATTTNCTNNGCCCGGTCNCGCNTNNGTC--CCNCCCGGCTCCGGAA
1060 1070 1080 1090 1100 1110 1120
AAACGAGGCAAGAGTTCCTCCCGGTAGGCACTGGAGCAATGCTGATGCTCCGGATGCTGCAGACTCGG
1130 1140 1150 1160 1170 1180 1190
NTNCACCCCGGAAANNCTNNCNAACNAATTCGGAATAATTCCTCCNNTNCCTCAATTCCTCCCNAGACTN
1200 1210 1220 1230 1240 1250 1260
ACAGGATTCGTCACATTTGATGACATGAGTCTCTAGCAGCAAGGCTGTTGTACTCTGGTGGCGGTA
1270 1280 1290 1300 1310 1320 1330
TCCTCNANCNCAATTTTCTTTTNTCA---CGAACNCGNCCNNAATAATGNNNNNCCCTCCNCTNGTC
1340 1350 1360 1370 1380 1390 1400
CGGAGAGCTGGCTCCACCATCTGCTCCCTGGCTCTTGGTCCGCTCAAGACTGTGCAGC
1410 1420 1430 1440 1450 1460 1470
CNAATCNCCANC
1480 1490 1500
740 750

5. US-09-030-606-177' (1-1119)
US-08-904-809-39 Sequence 39, Application US/08904809

Initial Score = 60 Optimized Score = 217 Significance = 2.43
Residue Identity = 30% Matches = 233 Mismatches = 513
Gaps = 9 Conservative Substitutions = 0

140 150 160 170 180 190 200 210
TCCAGGAGCTCTGAGGTGGTTGTCATGAATGGACAGCATACACTAAATGAAGAAATGCTAGACCTGCCCTGGT
220 230 240 250 260 270 280
GTACTGACATGAGGATTTAAAGCTTTGGTAAATGGAAACACAGCATCATCATTCATTCATGACCTGCA
290 300 310 320 330 340 350
CACATTTAATTTTATTTGATTTTAAATGCTGTCACAAACAATATTTATTCATTTGTTCTTTTAT
360 370 380 390 400 410 420
CAGCATCTTGAAGAGCTPATATGATCCCTCACCTGTAGTCAAGAGAAATGTTGGGAAATGCTGACACTGA
430 440 450 460 470 480 490
AGCAGGAAATCTCAATTCAGTGAGGATAACTGGATACCAAGATGGTTGAGGCCAAGTACGCTAATTTCCAC


```
CAGCATCCTTGAAGAGCTATATGATCCTCACCCTCTGTAGGTGAGAAATATATGGAATGGCTGACACTGA
|||||
TTCCTTTTCTGTAGGCGCCTTAAGCTTTCTAAATTTGGAACTTAAGCAAGCTGAAGGAAAGGGGCT
170 180 190 200 210 220 230
430 440 450 460 470 480 490
AGCAGGAAATCTCAATTCAGTGAAGATAACTGGATACCAAGAGTTGTAGGCCCAAGTACGCTAATTTCCAC
|||||
TTCGCAAAATCACTCGGGGGAAGAAAGTTGCTTTGTTAAATCATGCCCTATGGTGGGTGAATCACTGTT
240 250 260 270 280 290 300 310
GTACAATTACNTTTCACCTTTTAATTAATTTGCTNAANGCTTTAATTAACCTTGGGGTTCCTCCCCANAC
320 330 340 350 360 370 380
500 510 520 530 540 550 560 570
TAAACATCGGCGATGTTAGTACATAGACAGCAGTCAACAGTATCATGATGATGATGATGATGATGATG
|||||
CTATGGTCTGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
580 590 600 610 620 630 640
CAACCCCNCTGACAAAAGTCCCGCCCTCAATNATGTCGGGCTCAATNATGTCGGGCTCAATNATGTCGG
390 400 410 420 430 440 450
650 660 670 680 690 700 710
CAGCAGACGCTCTTGTGACTGGAAGTTGCGG-----AAATGGTACAACTGATGATGATGATGATGATG
|||||
CTCATTTNCCCNCCAGTNNAAATGAAGGTTACCATNTTAAACNCCACTCCACCTCCACCTCCACCTGGA
460 470 480 490 500 510 520
720 730 740 750 760 770 780
CACACTCCAGCCTCCACAGTCTGGGCTGGAATGCAATCAGAGCATGCTGCGGAGAGAGAGAGAGAGAG
|||||
ATCCTCNAAANCCCTCAACNAAATNCTNNGCCCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGAA
530 540 550 560 570 580 590
790 800 810 820 830 840 850
AAACGAGGCAAGAGTTCCCGCGGTGAGGCAATGCGAAGCAATGCTGATGCTCGGATGCTGCTGCTGCTG
|||||
NTNCACCCCGGAGANNCTNNAACNAAATCCGAAATATCCGAAATATCCGAAATATCCGAAATATCCGAA
600 610 620 630 640 650 660
860 870 880 890 900 910 920
ACACGAGGCTCGTCAACTGATGAGTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG
|||||
TCCTCNCCNCCNCAATTTCTTTNTCA---CGAACGNNCCNNAATGNNNNCCCTCCCTCCCTGCTGTC
670 680 690 700 710 720 730
930 940 950 960 970 980
CGGAGAGGCTCGGCTCCACCATCTGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
|||||
CNNAATCNCCANC
740 750
```

6. US-09-030-606-177' (1-1119)

US-09-020-747-39 Sequence 39, Application US/09020747

Initial Score = 60 Optimized Score = 217 Significance = 2.43
Residue Identity = 30% Matches = 233 Mismatches = 513
Gaps = 9 Conservative Substitutions = 0

```
140 150 160 170 180 190 200 210
TCCAGGAGTCTGAGGTGGTTCATGATGAGCAGCATACACTAAATGAGAATGCTAGACCTGCCCTGGT
|||||
220 230 240 250 260 270 280
GTACTGAGCATGAGGATTTAAAGCTTTGGGTAATGGGACAGCATACATCATGATGATGATGATGATGATG
|||||
CACATTAATTTTATTTGATTTTATTTTAAATGCTGCACACACAAATATTTATTTATTTGTTCTTTATT
30 40 50 60 70 80 90
```

```
290 300 310 320 330 340 350
CACCCACCTGGGAGGTCCAGAGGGCGCACCTTTTACACAGAGGAGAAATGAATTTGTGAGGGAGTAC
|||||
TCATTTTATTTGTTAGTCTGCTGCTTTTATTTTATTTTACTGAAAGTGAGAGGAACTTTTGTGGCCTTTT
100 110 120 130 140 150 160
360 370 380 390 400 410 420
CAGCATCCTTGAAGAGCTATATGATCCCTCACCTCTGTAGTCAAGAAATATTTGGGAATGGCTCACACTGA
|||||
TTCCTTTTCTGTAGGCGCCTTAAGCTTTTCTAAATTTGGAACATCTAAGCAAGCTGAANGGAAAGGGGT
170 180 190 200 210 220 230
430 440 450 460 470 480 490
AGCAGGAAATCTCAATTCAGTGAAGATAACTGGATACCAAGAGTTGTAGGCCAAGTACGCTAATTTCCAC
|||||
TTCGCAAAATCACTCGGGGGAAGAAAGTTGCTTTGTTAAATCATGCCCTATGGTGGGTGATTAAGTCTT
240 250 260 270 280 290 300 310
500 510 520 530 540 550 560 570
TAAACATCGGCGATGTTAGTACATAGACAGCAGTCAACAGTATCATGATGATGATGATGATGATGATG
|||||
GTACAATTACNTTTCACCTTTTAATTAATTTGCTNAANGCTTTAATTAACCTTGGGGTTCCTCCCCANAC
320 330 340 350 360 370 380
580 590 600 610 620 630 640
CTATGGTCTGGCTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG
|||||
CAACCCCNCTGACAAAAGTCCCGCCCTCAATNATGTCGGGCTCAATNATGTCGGGCTCAATNATGTCGG
390 400 410 420 430 440 450
650 660 670 680 690 700 710
CAGCAGACGCTCTTGTGACTGGAAGTTGCGG-----AAATGGTACAACTGATGATGATGATGATGATG
|||||
CTCATTTNCCCNCCAGTNNAAATGAAGGTTACCATNTTAAACNCCACTCCACCTCCACCTCCACCTGGA
460 470 480 490 500 510 520
720 730 740 750 760 770 780
CACACTCCAGCCTCCACAGTCTGGGCTGGAATGCAATCAGAGCATGCTGCGGAGAGAGAGAGAGAGAG
|||||
ATCCTCNAAANCCCTCAACNAAATNCTNNGCCCGGTCGCGGTCGCGGTCGCGGTCGCGGTCGCGGAA
530 540 550 560 570 580 590
790 800 810 820 830 840 850
AAACGAGGCAAGAGTTCCCGCGGTGAGGCAATGCGAAGCAATGCTGATGCTCGGATGCTGCTGCTGCTG
|||||
NTNCACCCCGGAGANNCTNNAACNAAATCCGAAATATCCGAAATATCCGAAATATCCGAAATATCCGAA
600 610 620 630 640 650 660
860 870 880 890 900 910 920
ACACGAGGCTCGTCAACTGATGAGTGAAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG
|||||
TCCTCNCCNCCNCAATTTCTTTNTCA---CGAACGNNCCNNAATGNNNNCCCTCCCTCCCTGCTGTC
670 680 690 700 710 720 730
930 940 950 960 970 980
CGGAGAGGCTCGGCTCCACCATCTGGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG
|||||
CNNAATCNCCANC
740 750
```

7. US-09-030-606-177' (1-1119)

US-09-020-747-17 Sequence 177, Application US/09020747

Initial Score = 60 Optimized Score = 148 Significance = 2.43
Residue Identity = 34% Matches = 158 Mismatches = 294
Gaps = 4 Conservative Substitutions = 0

```
620 630 640 650 660 670 680
GTTTAGGTGAATTAGCGTCACTTGGCCTCAACCATCTTGGTATCCAGTATCTCTCACTGAATGAGATTTC
|||||
X 10 20
TTTTTTTTTTTTTTTAAACATCA
```


[illegible]

GC

US-09-030-606-177' (1-1119)
US-09-020-747-11 Sequence 110, Application US/09020747

CAGCTTCGTTTATTAAACCACTTAATGTGTTTCAACTGCACATCCCATTGAACCATGGGCCCTCTCCCTC
 30 40 50 60 70 80 90
 1111 1111 1 11 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111 1111
 CAGCAGGTGTTGAGCATG-GCCTCAGAAGCTGCACCGGCACCAAGGGCTGGCACAATGGGCCCTTGCTG
 100 110 120 130 140 150 160

100 110 120 130 140 150 160
ACCTCCCAAGGAGGAGCATGACAGAGCTCAACTAGGCGAGAATCCAGGAGTCCTGAGGTGGTTGCATCA
170 180 190 200 210 220 230
ATTCTTAGGCAGTTGGCGGACGCAAGGAGGAGGCGCGAGCTCTCTGGAGCAGAGCCGA-GACCAAGCAGTT
170 180 190 200 210 220 230
ATGGCAGCATACACTAAATGAAGAATGCTAGACCTGCCCTGGTGTACTGAGCATGAGGATTAAGAGCT
CTGAGTGCCTGAACGCCGCCCTGA---GCCCTACCG-CTTGGCCCACTATGTTGCAGAGGCTGTGGTGA
240 250 260 270 280 290 300
TTGGTAAATGGGACACGATCATATTCTATTGTGACCTGACACCCACCTCGGAGGCTCCAGAGGCG
GCCGCTGTGCGGCACCGGAAGCCAGCTCTTCTGTGTCAACCTGTAACCTTTGGSCCTGGAGGTGTGT
310 320 330 340 350 360 370
GCACCTTTCCTACTACACAGGAGAAATGATTTGTGAGGGAGTACCAGCATCTTGAAGAGCTAATGATCC
TTGGTAAATGGGACACGATCATATTCTATTGTGACCTGACACCCACCTCGGAGGCTCCAGAGGCG
380 390 400 410 420 430 440
TTGGCGGACGATCATCTATGTGCGCGCTCTCTCTGGAATGGGGGTAGAGAGAAGTTTCATGACCATGG
CTCACCTCTGTAGTGCAGAAATATGTGGAAATGCTGACACTGAGCAGGAATCTCAATTGAGTGAGGAT
450 460 470 480 490 500 510 520
TGCTGGGCATTGGTCAGTGTGGGCTGGTCTGTGTCCTGCTCTAGGCTCCTAGGCTACGCCAGTGACCACTGGCGTG
AATGTGATACCAAGATGTTGAGGCCAAGTGACGCTAATTTCACTTAAACATCGGCATGTTAGTACAATAG
GAGCTATGGCGCGCGCGCCCTTCATCTGGGCATCTCTTGGGCATCTGCTGAGCCCTTTTCTCATCC
530 540 550 560 570 580 590
530 540 550 560 570 580 590
ACAGCAGCTCAACACAGATATCATGATAGTCTGACITCGAGAACTATGGTGTGCG-TAGTTGATCACAG
CAAGGCGCGCTGGCTAGCAGGCTGTCTGCCGGATCCAGGCCCTGGAGCTGCACTGCTCATCTCTCC
600 610 620 630 640 650 660
600 610 620 630 640 650 660
TGTTCCGGGTGATG-----CAGTGAGCAGTAGTG--AGCACCCAGTGAGGATGACGAGCAGCTCCTTGAC
CGCTGGGGCTGCTGGACTCTGTGGCCAGGTGTGCTTCACTTCACTGAGGCCCTGCTCTGACCTCTCC
670 680 690 700 710 720 730
670 680 690 700 710 720 730
TGGAAATGGCCGAATGTACAACTTCG-CAGGGTGGGAAGACTTCTCACTCCCGAGGATGACGAGTCCACAGTC
GGACCCGGACCACTGTCCGAGGCTACTCTGTATGCTTTCATGATCAGTCTTTGGGGGTGCTGGGCT
740 750 760 770 780 790 800
740 750 760 770 780 790 800
TGGGACTGGATGGCAATCACAGCATGTTGCCAGCAGACCC--AGCCAGAAACGAGCAGAGATTCCTCCCG
ACCTCTCGCTGCCATTGACTGGACACAGTAGCCCTGGCCCTTCTGATGCTTTCATGATCAGTCTTTGGGGGTGCTGGCTCT
810 820 830 840 850 860 870 880
810 820 830 840 850 860 870 880
CGGTAGGCACTGGGAAGCAATGCTGATGCTCCGGATGTTGCAGACTCGACACGATTCGTCACACTGA
TTGGCTCTCACCTCATCTTCTTCACTTCGTAGCAGCCACACTGCTGTGGTGTGGGAGGACGCGTGG
890 900 910 920 930 940 950
890 900 910 920 930 940 950
TGAGCATGAGTCTGTAGCGACGAAGGTCTGTGTACTCTGGTGCCCTACGAGAGGCTGCGCTCCACCA
GCCCCACGAGCCAGCA--GAAGGGCTTGGGCCCTCTTGTGCCCCACTGTCTTCATGCCCGGCCG
960 970 980 990 1000 1010 1020
960 970 980 990 1000 1010 1020
950 960 970 980 990 1000 1010 1020

[illegible]

10. US-09-030-606-177' (1-1119)

US-09-020-747-79 Sequence 79, Application US/09020747

Initial Score	Residue Identity	Gaps
---------------	------------------	------

[illegible]


```
ACTAGTCCAGTGTGGTGAATTCAT
X      10      20
80      90      100      110      120      130      140
TGAACATGGGCTCTCCCTCACTCCCAAGGAGGAGCAGCATGAGGAGTCAACTAGGAGAGAAATCCAG
|||||
TGCTTTGGGGCTCTCACTCCCTCTCTCTGCA-GCTCCAGCTTGTCTCTGCTCTGAGAGACCAATGGCC
30      40      50      60      70      80      90
150      160      170      180      190      200      210
GAGTCCTGAGGTGGTTCATGAATGGAGCAGCATACACTAAATGAAGAAATGCTAGACCTGCCCTGGGTACT
|||||
CAGCATCTGAGTACCTCTGCTCTCTGCTGACACCTAGCTGTGGCCCTGGCTGGAGCCCAAGAGGAG
100      110      120      130      140      150      160
220      230      240      250      260      270      280
GAGCATGAGGAAATTAAGGCTTTGGGTAATGGGAACACGATCATATTCATCTGTCACCTGCAACCC
|||||
GATAGGATAATCCGGGTGGCATCTATAACGACAGACCTCAATGATGAGTGGGTACAGCGTCCCTTCACTTC
170      180      190      200      210      220      230      240
290      300      310      320      330      340      350      360
ACCCCTGGAGGCTCCAGAGGGCGCACCTTTCACTACACAGAGAAATGTAATTTGAGGGGAGTACCAACA
|||||
GCCATCAGCGAGTATAACAAGGCCACCAAGATGACTACTACAGAGCT---CCGCTCGGGGTACTAGAGGCC
250      260      270      280      290      300      310
370      380      390      400      410      420      430
TCCTTGAAGAGCTATATGATCCCTCACTCTGTAGTCAAGAAATATGTGGGAATGGCTGACACTGAAGAG
|||||
AGGCAACAGACCGTGGGGGGTGAATTAATCTCTCGACGTAGAGGTGGCCGCAACCATATGTACCAAGTCC
320      330      340      350      360      370      380
440      450      460      470      480      490      500
GAATCTCAATTCAGTGAGGATAACTGGATACCAAGATGGTTGAGGCCAAGTCACTGATTTTCACTAAAC
|||||
CAGCCCAACTTGGACACCTGTGCTTCCATGAACAGCCAGCAACTGCAAGAGAACACGTGTGCTCTTTCGAG
390      400      410      420      430      440      450
510      520      530      540      550      560      570
ATCGCATGTTAGTACAATAG-ACAGCAGCTCAACACAGTAATCATGATGCTGACTTCGGAGAACTAT
|||||
ATCTACGAAGTTCCTGGGAGAGACAGAAAGTCCCTGGGTGAATCCAGGTGCAAGAAATCCTTANGATCT
460      470      480      490      500      510      520
580      X      590      600      610      620      630
GGTGTGGCTAGTGTATGATCACAGTGTCCGGGTGATGAGTGAAGTGTGAGCAGTGTGAGCACCCAG
|||||
GTTGCCAGGC
530      X
```

15. US-09-030-606-177' (1-1119)

US-08-904-809-74 Sequence 74, Application US/08904809

Initial Score = 54 Optimized Score = 174 Significance = 1.96
Residue Identity = 36% Matches = 203 Mismatches = 331
Gaps = 20 Conservative Substitutions = 0

```
180      190      200      210      220      230      240      250
CACTAAATGAAGAAATGCTAGACCTGCCCTGGTGTACTGAGCATGAGGGATTTAAAGGCTTTGGGTAAATGGG
|||||
TTTCATAGGAGAACACACTGAG
X      10      20
260      270      280      290      300      310      320
AACACGATCATACATTCATATTGTGACCTGACACCCCTGGAGGCTCCAGAGGGCGGCACTTCTACT
|||||
GAGATCTTGAAGAATTTGGATTTCAGCCGCGAGAGATTTATCAGCTTACTCAGATAAAATCATTTGAAGT
30      40      50      60      70      80      90
330      340      350      360      370      380      390
ACAACAGGAGAAATGAATTTGTGA-GGGGAGTACCAGCATCTTGAAGACTATATGATCCCTCACTCTGT
|||||
AATAAGGTAAAGCTAGTCTCTAACTTCCAGGCCCGGCTCAAGTGAATTTGAATCTGCAATTCACAGTGT
100      110      120      130      140      150      160
400      410      420      430      440      450      460
AGTCAAGAAATTAATGTGGGAATGGCTGACACTGAAGCAGGAAATCTCAATTCAGTGAAGATACTGGTATACC
|||||
AGAGTAACACATAACATTTGATGATGATGGAACATGGAGGAA-----CAGTATTACAGTGTCTCTCACTCTGT
```

```
100      110      120      130      140      150      160
AATAAGTAAAGCTAGTCTCTAACTTCCAGGCCACGCTCAAGTGAATTTGATTTTCAATTTACAGTGT
|||||
400      410      420      430      440      450      460
AGGTCAAGAAATTAATGTGGGAATGGCTGACACTGAGCAGGAGAAATCTCAATTCAGTGAAGATACTGGATACC
|||||
AGAGTAACACATAACATTTGATGATGATGGAACATGGAGGAA-----CAGTATTACAGTGTCTCTCACTCTGT
170      180      190      200      210      220      230
470      480      490      500      510      520      530
AAGATGCTTCCAGGCCAAGTCAAGCTAATTTCACTTAACATCGCATGGCTGTAGTACATACTAGACAGCAGTC
|||||
AATCAAGAAAGAAATTAACAGACTCTGATTTCTACAGATGATGATTAATTCATAAAATGATATCAATCAATTA-GGGC
240      250      260      270      280      290      300
540      550      560      570      580      590      600
AACACAGTAACTATGATAGTCTGACTTCGGAGACTATGCTGGCTAGTGTATCATCAGCTGTCCCGGTGA
|||||
TTTTGATTTAANACTTTGGGTACTTATATACTAAATATGATGATGCTTCCAGCTTCCAGTTCTTGATAT
310      320      330      340      350      360      370
610      620      630      640      650      660      670      680
TGCAGTGAAGTGTGAGCAGCCAGTGAAGTGCAGCAGAGCTCTCTGCACTGGAAGTTGCCGAATGCT
|||||
ATTGTTGATTTAAGATTTCTTGACTTATATTTTGAATGGTCTTACTGAAAANG-----AATGAT
380      390      400      410      420      430
690      700      710      720      730      740      750
ACAACCTGCGCAGGTTGGAAAGCTTCTCACACTCCAGCTCCACAGCTGCGGACTGGGACTGGATGGCAAT--C
|||||
ATATCTTGAAGACATCGATATACATTTTATTTTACACTCTTGTATCTACAATGTAGAAAATGAAGAAATGCC
440      450      460      470      480      490      500
760      770      780      790      800      810      820
ACAGCATCTGTTCCCGCAGCAGACCCAGCCAGAGGAGGAGTTCGCCGGGTGAGGCACTGCCGAAGA
|||||
CCAAATTTGATGTGATAAAGTCCCGT
X
510      520      530
```

ATGCTG

16. US-09-030-606-177' (1-1119)

US-09-020-747-74 Sequence 74, Application US/09020747

Initial Score = 54 Optimized Score = 174 Significance = 1.96
Residue Identity = 36% Matches = 203 Mismatches = 331
Gaps = 20 Conservative Substitutions = 0

```
180      190      200      210      220      230      240      250
CACTAAATGAAGAAATGCTAGACCTGCCCTGGTGTACTGAGCATGAGGGATTTAAAGGCTTTGGGTAAATGGG
|||||
TTTCATAGGAGAACACACTGAG
X      10      20
260      270      280      290      300      310      320
AACACGATCATACATTCATATTGTGACCTGACACCCCTGGAGGCTCCAGAGGGCGGCACTTCTACT
|||||
GAGATCTTGAAGAATTTGGATTTCAGCCGCGAGAGATTTATCAGCTTAACTCAGATAAAATCATTTCAAGT
30      40      50      60      70      80      90
330      340      350      360      370      380      390
ACAACAGGAGAAATGAATTTGTGA-GGGGAGTACCAGCATCTTGAAGACTATATGATCCCTCACTCTGT
|||||
AATAAGGTAAAGCTAGTCTCTAACTTCCAGGCCCGGCTCAAGTGAATTTGAATCTGCAATTCACAGTGT
100      110      120      130      140      150      160
400      410      420      430      440      450      460
AGTCAAGAAATTAATGTGGGAATGGCTGACACTGAAGCAGGAAATCTCAATTCAGTGAAGATACTGGTATACC
|||||
AGAGTAACACATAACATTTGATGATGATGGAACATGGAGGAA-----CAGTATTACAGTGTCTCTCACTCTGT
```


[illegible]

18. US-09-030-606-177' (1-1119)
US-08-904-809-32 Sequence 32. Application US/08904809

Initial score	=	54	Optimized Score	=	242	Significance	=	1.96
Residue Identity	=	34%	Matches	=	288	Mismatches	=	497
Gaps	=		Conservative Substitutions	=	43		=	0

[illegible]

TGACAGTGGGGCTTCCTCCACTCCCCAAGGAGGCAGCATCGAGGAGCTCAACTAGGCGAGAATCCAG
— — — — —
GGCAGGTTTATTGACAACCTCNCGGGACACAAACAGGTGGGGACAGGCGGAACAGGCTCCGGCGGGCGGC

150 160 170 180 190 200 210
GAGTCTGAGGTGGTTCATGAATGGACAGCATACACTAAATGAAGAAATGCTAGACCTGCCCTGGTGTA
GGCGGGCGCCCTACTTGC-----GATACCAATATGCAGCTCCGCTCCGGCTTGATTTCCCTCTGCAGCTG

GAGCATGAGGGATTTAAAGGCTTTGGGTAAATGGGAACACCATCATTCATTCATTTGTGACCTGCACACCC

170	180	190	200	210	220	230
470	480	490	500	510	520	530
AAGATGGTTGAGCCCAAGTGCACGCTAAATTTACCTAAACATCGCATGGTTAGTACAATAGACAGCACAGTC						
AATCAGAAAAAGAAATTACAGACTCTGATCTTACAGTGATGATTTCTAAAAATGGTAATCATTTA -GGGC						
240	250	260	270	280	290	300
540	550	560	570	580	590	600
AACACAGTAATCATGATAGTCTGTGACTTCGGAGAACTATGGTGTCTGCTAGTTGATCACAGTGTTCGGGTGA						
TTTTGATTATTAANACTTTGGGTACTTATTAATAATATGGTAGTTATCTGCTTCACAGTTTGCCTTGATAT						
310	320	330	340	350	360	370
1610	620	630	640	650	660	670
TGCAGTGACGAGTAGTGACACCCACTGAGGATGCAGCAGGACGCTCCTTGCATCGGAAGTTGCCGAAGATGGT						
ATTGTGTGATATTAAAGATTCTTGCACTTATATTTTGAATGGGTTCTACTGAAAANG-----AATGAT						
380	390	400	410	420	430	
690	700	710	720	730	740	750
ACAACCTGCCAGGGTTGGGAAGCTTCTACACTCCGACCTCCACAGCTCTGGGACCTGGATGGCAAT--C						
ATATCTTGAAGACATCGATATACATTTATTTACACTCTTGATCTACAAATGAGAAATGAAGAAATGCC						
440	450	460	470	480	490	500
760	770	780	790	800	810	820
ACAGCATCGTTCCGACGACACCCCGAGCCAGAACGAGCTCCCCCGGTAGGCGCACTGCGCAGCA						
CCAAATTGTATGTGTGATAAAAGTCCCGGT						
510	520	530	540	550	560	570

17. US-09-030-606-177' (1-1119)
US-08-806-596-32 Sequence 32, Application US/0806596

Initial Score	=	54	Optimized Score	=	242	Significance	=	1.96
Residue Identity	=	34%	Matches	=	288	Mismatches	=	497
Gaps	=	-	43	Conservative Substitutions	=	-	=	0

[illegible]

80 90 100 110 120 130 140
 TGAACCATGGGGCCCTCTCCCTCACTCCCCAAGGAGGAGCATCGAGGCTCAACTAGCGCAGAGAACTCAG
 GGCGATGTTTATTGACAACCTTCMGSGACACACAACAGGCTGGGGACAGCGGCAACAGGCTCGGGGGGGCGC

150 155 160 165 170 175 180 185 190 195 200 205 210
 GAGTCTCAGGTGGTTGCATGAATGGACAGCATACACTAAATGAAGAAATGCTAGACCTGCCCTGGTGACT
 GCGCGCGGCCCTACCTGC-----GATCAAAATGTGACCTCCGCTCCGCTGATGATTTCCCTCGACGTG

GAGCATGAGGATTAAAGCGTTTGGSTAAATGGACACGATCATACATTTCATCTGTGCCTGCACACC
||| || | ||| || ||| -----TGGCACCTGGGATTNNAATT
CAGGATGCCNTAAACAGGCGCTCGCCNTNG-----

220 230 240 250 260 270 280

[illegible]

TAGACACAGCTCACACAGATCATGACTGTGACTTCGGAGAACTAATGGTCTGGCTAGTTGATCACC
|||||
TGGAGAAGAGGCCCAAAAAGAACCTGTTCTGCAGTGAATGGGATTAATAATGCTCTTAGTAGCCACA
|||

440	450	460	470	480	490	500
820	830	840	850	860	870	880

[illegible]

23. US-09-030-606-177' (1-1119)
US-08-904-809-28 Sequence 28, Application US/08904809

Initial Score	=	51	Optimized Score	=	203	Significance	=	1.72
Residue Identity	=	31%	Matches	=	237	Mismatches	=	490
Gaps	=		Conservative Substitutions	=	21		=	0

G T R A T G G A C A C G A T A C A T T C A T C T G A C C T G C A C C C A C C C T G G A G G C T C A G A G G G C G A C
|| || | || |
A G G A A G G C C G A G G G A T A T T G T

320 330 340 350 360 370 380
CTTTCACACAGCAGGAATTAATTGTGAGGGGATCCAGCATCCTTTGAAGAGCTATATGATCCCTCA

ANGGGATTGAGGGATAGGAGNATAANGGGGAGGTGTCTGCCAACATGANGCGTCNNCTCTCTCTCTCTCTCTCT

[illegible]

60 470 480 490 500 510 520 530
GGATACCAAGATGGTTGAGGCCAAGTACGGCTAAATTTCACCTAAACATCGGCATGGTTACTACAANTAGACAG

GATTTTCGGCTCTTATTCAGTATNTANATTCCTCTNAATCGAAATNATNTTTCNCGGAAATTTGGCT
 160 170 180 190 200 210 220
 CACAGTCACACAGTATTCATGATAGTCTGACTTCGAGAACTATGCTGCTGGCTAGTATGATTCACACAGGCTC
 540 550 560 570 580 590 600

[illegible]

680 690 700 710 720 730 740
 ---TAAAGNTTNAAGTGGGANTNCAAATGAAACCCCTNNCACAGAGNATCCNTACCGCACTCTGTTTTNNCTCT
 310 320 330 340 350 360 370
 5'-TAAAGTACACACAGTGGAGTATGAGCAGGACGTCCTTGTGCACCTGGGAAGTGTGCC

380 390 400 410 420 430
 CGCCCTTCTGACTCTGCGNCGAGCCCAATACCCGNGNGNATGTCNC-----CGNNGNNGCGNCTGAAANN
 AAATGGTACAAACCTGCCAGGTTGGGAAGCTTCTCACACTCCGAGCTCCACAGTCTGGGACTGGATGG

750	760	770	780	790	800	810
CAATCAGCATCGTTCCGCA--GCAGACCCAGCCAGAACAGGAGGAGAGTTC						
NCTCGNGGCTNNGANCATCANGGGTTTCGATCAAAGNCNGTTCNCATNAAGCACTATTNGCCTCAT						
440	450	460	470	480	490	500
820	830	840	850	860	870	880
CGAAGCAATGCTGATGCTCCGAT--GGTGTCAGACTCGGACACGATTCGTCCAACATTGATGACATGAGGT						
CCAACCNTNSCCCTCNCCATTTNGCGTCNGGTCNCCTACGCTNNINGCNCCTNNNTNGANATTTTNC						
510	520	530	540	550	560	570
890	900	910	920	930	940	950
CGTTAGCGAGCAAGGGTCTGTTGTACTGSGGCCGTACGGRAGGCTGGCTCCACCATCTGGGCTCCGTG						
CGCTNGSGGAANCCCTCTGNAATGGGTAGGNCCTTNTCTTTTNAOCNNNGGTTACTAATCNNCTNCACG						
590	600	610	620	630	640	650
960	970	980	990	1000	1010	1020
GCT-CTTGGTGGGCTCAAGACTGTGCAGGCCAGCCGATGTTAGAGTTCTCGAAACAGTGTGGCGGT						
CNTNCTTCTCNACCCCCCCCCTTTTCAATCCACNGGCCNAATGGGCTCTCCCNCCGANGGGGGNNCC						
660	670	680	690	700	710	720
x	1050	1060	1070	1080		
GACAGCACCCACTGCGGATGCACCGAGGACGCCGAGCAGACAATTCGTTTCCAT						
CANNCC						
730						

24. US-09-030-606-177' (1-1119)

US-08-904-809-47 Sequence 47, Application US/08904809

Initial Score	=	50	Optimized Score	=	256	Significance	=	1.65
Residue Identity	=	37%	Matches	=	295	Mismatches	=	470
Gaps	=		Conservative Substitutions	=				

220 230 240 250 260 270 280
 TGGCATGGGGATTAAAGCCTTTGGGTAAATGGGAACAGATCATCATTCATTGTCACTGCACACCC
 ||| |||
 ACAGGGGGCATATATGAAGGAG
 X 10 20

[illegible]

160
A-----TCCTTGAAGAGCTATATGATCCCTCACCCTGTAGTGCAGAATAATTATGTGGGA-ATGGCTTGACACT
 | | | | | | | | | | | | | | |
 | | | | | | | | | | | | | |
ATAAATTTCCTTTGGGGAGGTTCAAGAGCGTTTCACTGTCTTGGAACTTTAATATCCATCTGCTGCCGACGATTAATGATTT

GAAGCAGCAATCTCAATTGAGGTAACTTGGA-TACCAGAATGTTGAGCCCAAGTGACGCATAATTC
 430 440 450 460 470 480 490

170 180 190 200 210 220 230
 ATTGACCCCTGAGGGCATATACACAGCGGACTCTGGGAGGAGGATTAACAGAAAGGGCACAAAGGCTTAATCCCT
 500 510 520 530 540 550 560
 ACCTTAACATCGGCATGGTTAGTACAAATAGACAGACACAGTCAACACACAGTAATCATGATGACTGTGACTTCGGGA

AAAAAATCAAGAAAGGAGGTGGGTATACCTCCAGGCTACAGTGTCTCCAG-----GGCTCTCTCT
 240 250 260 270 280 290 300
 GAACTATGGTCTAGTCTGATCATCAGATCTCCGGTATGTCAGTGCAGCATCTACTGAGCACCACGACG
 310 320 330 340 350 360 370 380 390 400

CATCCCTGGAGGACGACAGTGGAGGACAACACTGACCATGTCCACAG---GCTCCTGTGTGGTGGCTCTCTGGT
310 320 330 340 350 360 370

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